

118027

From: Hutzell, Paula  
Sent: Monday, March 29, 2004 8:30 AM  
To: Holleran, Anne; STIC-Biotech/ChemLib  
Cc: Chan, Christina  
Subject: RE: RUSH sequence search for 09/477,082

approved

-----Original Message-----

From: Holleran, Anne  
Sent: Friday, March 26, 2004 12:02 PM  
To: Hutzell, Paula  
Cc: Chan, Christina  
Subject: FW: RUSH sequence search for 09/477,082

-----Original Message-----

From: Holleran, Anne  
Sent: Friday, March 26, 2004 12:01 PM  
To: Chan, Christina  
Subject: RUSH sequence search for 09/477,082

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following for 09/477,082

interference databases **only** search of SEQ ID NO: 1(na)  
interference databases **only** search of SEQ ID NO: 2(na)

commercial and interference database search of SEQ ID NO: 29, 30, 31, 32, 33, 34(na), these are primer sequences *Please perform a Score/Length sequence search for the primer sequences (SEQ ID NO: 29-34) with a minimum hit length of 15 and a maximum hit length of 40, and a score over length value of 90% or greater*

SEQ ID NO: 1 and SEQ ID NO: 2 are two different regions of the same gene

Anne Holleran  
AU: 1642  
Tel: (571) 272-0833  
RM: Remsen, 3A14

mailbox: Remsen, 3C18

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 3/31  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 12:49:34 ; Search time 2672.94 Seconds				
(without alignments)				
10864.389 Million cell updates/sec				
Title: US-09-477-082-1				
Perfect score: 670				
Sequence: 1 aagcgctccaagacacgatt.....gggggttaaataaagcgcttt 670				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 3470272 seqs, 21671516995 residues				
Total number of hits satisfying chosen parameters: 1364278				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : GenEmbl:*				
1: gb_ba:*				
2: gb_htg:*				
3: gb_in:*				
4: gb_om:*				
5: gb_ov:*				
6: gb_pat:*				
7: gb_ph:*				
8: gb_pl:*				
9: gb_pr:*				
10: gb_ro:*				
11: gb_sts:*				
12: gb_sy:*				
13: gb_un:*				
14: gb_vi:*				
15: em_ba:*				
16: em_fun:*				
17: em_hum:*				
18: em_in:*				
19: em_mu:*				
20: em_om:*				
21: em_or:*				
22: em_ov:*				

23: em_pat:*						
24: em_ph:*						
25: em_pl:*						
26: em_ro:*						
27: em_sts:*						
28: em_un:*						
29: em_vi:*						
30: em_htg_hum:*						
31: em_htg_inv:*						
32: em_htg_other:*						
33: em_htg_mus:*						
34: em_htg_pln:*						
35: em_htg_rod:*						
36: em_htg_mam:*						
37: em_htg_vrt:*						
38: em_sy:*						
39: em_htgo_hum:*						
40: em_htgo_mus:*						
41: em_htgo_other:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
5313	13.4	2	15	6	AR208417	0.893333
c5314	13.4	2	15	6	AX802132	0.893333
5315	13.4	2	15	6	BD208917	0.893333
8164	13	1.9	15	6	AX009449	0.866667
c1846	14.4	2.1	17	6	AX758412	0.847059
1847	14.4	2.1	17	8	ATH526809	0.847059
1848	14.4	2.1	17	8	ATH526810	0.847059
5316	13.4	2	16	6	AR080878	0.8375
c5317	13.4	2	16	6	BD266396	0.8375
c5318	13.4	2	16	6	BD104574	0.8375
1082	15	2.2	18	6	AX378655	0.833333
15795	12.4	1.9	15	6	A52100	0.826667
15796	12.4	1.9	15	6	A52101	0.826667
15797	12.4	1.9	15	6	A52128	0.826667
15798	12.4	1.9	15	6	A52129	0.826667
15799	12.4	1.9	15	6	A65237	0.826667
15800	12.4	1.9	15	6	A66708	0.826667
15801	12.4	1.9	15	6	A66711	0.826667
15802	12.4	1.9	15	6	A68206	0.826667
15803	12.4	1.9	15	6	A68260	0.826667

← No hits score/length  
90% or above

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: March 29, 2004, 11:54:58 ; Search time 289.564 Seconds						
(without alignments)						
9829.571 Million cell updates/sec						
Title: US-09-477-082-1						
Perfect score: 670						
Sequence: 1 aagcgctccaagacacgatt.....ggggtaaataaagcgcttt 670						
Scoring table: IDENTITY_NUC						
Gapop 10.0 , Gapext 1.0						
Searched: 3373863 seqs, 2124099041 residues						
Total number of hits satisfying chosen parameters: 2072792						
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 65000 summaries						
Database : N_Geneseq_29Jan04:*						
1: geneseqn1980s:*						
2: geneseqn1990s:*						
3: geneseqn2000s:*						
4: geneseqn2001as:*						
5: geneseqn2001bs:*						
6: geneseqn2002s:*						
7: geneseqn2003as:*						
8: geneseqn2003bs:*						
9: geneseqn2003cs:*						
10: geneseqn2004s:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
3719	14	2.1	15	4	AAH20313	0.933333
3720	14	2.1	15	6	ABK98147	0.933333

7279	13.4	2	15	3	AAZ64339	0.893333
c7280	13.4	2	15	4	AAH74112	0.893333
7281	13.4	2	15	6	AAD39760	0.893333
7282	13.4	2	15	6	ABX01392	0.893333
11340	13	1.9	15	3	AAZ48115	0.866667
c2401	14.4	2.1	17	6	ABN07749	0.847059
c2402	14.4	2.1	17	6	ABN07750	0.847059
c2403	14.4	2.1	17	9	ADB41410	0.847059
c17300	12.6	1.9	15	6	ABA03942	0.84
c7283	13.4	2	16	6	ABL31189	0.8375
1374	15	2.2	18	6	ABK41196	0.833333
21562	12.4	1.9	15	2	AAQ29530	0.826667
21563	12.4	1.9	15	2	AAQ81114	0.826667
21564	12.4	1.9	15	2	AAT55623	0.826667
21565	12.4	1.9	15	2	AAT31819	0.826667
c21566	12.4	1.9	15	2	AAX64708	0.826667
21567	12.4	1.9	15	2	AAT37116	0.826667
c21568	12.4	1.9	15	2	AAT50251	0.826667
21569	12.4	1.9	15	2	AAV07762	0.826667
21570	12.4	1.9	15	2	AAV07759	0.826667
21571	12.4	1.9	15	2	AAV06230	0.826667
21572	12.4	1.9	15	2	AAX33998	0.826667
21573	12.4	1.9	15	2	AAV06801	0.826667
21574	12.4	1.9	15	2	AAV48551	0.826667
21575	12.4	1.9	15	2	AAV06817	0.826667
21576	12.4	1.9	15	3	AAZ64338	0.826667
21577	12.4	1.9	15	3	AAA07813	0.826667
21578	12.4	1.9	15	4	AAH20310	0.826667
21579	12.4	1.9	15	4	AAF31459	0.826667
21580	12.4	1.9	15	4	AAF59902	0.826667
21581	12.4	1.9	15	4	AAF59905	0.826667
21582	12.4	1.9	15	4	AAF31566	0.826667
21583	12.4	1.9	15	4	AAF52237	0.826667
c21584	12.4	1.9	15	4	AAF52606	0.826667
21585	12.4	1.9	15	4	AAF52236	0.826667
c21586	12.4	1.9	15	4	AAF52607	0.826667
21587	12.4	1.9	15	4	AAH28548	0.826667
21588	12.4	1.9	15	4	AAF97971	0.826667
c21589	12.4	1.9	15	6	AAD41857	0.826667
21590	12.4	1.9	15	6	ABX01391	0.826667
21591	12.4	1.9	15	6	ABK98173	0.826667
21592	12.4	1.9	15	6	ABK98172	0.826667
21593	12.4	1.9	15	6	ABK98144	0.826667
21594	12.4	1.9	15	7	ABX16342	0.826667
21595	12.4	1.9	15	9	ADC66181	0.826667
21596	12.4	1.9	15	9	ADC66180	0.826667
c3721	14	2.1	17	7	ABT40012	0.823529
c3722	14	2.1	17	9	ADE25256	0.823529
1660	14.8	2.2	18	2	AAX03843	0.822222

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: March 29, 2004, 16:27:20 ; Search time 66.3879 Seconds						
(without alignments)						
5600.675 Million cell updates/sec						
Title: US-09-477-082-1						
Perfect score: 670						
Sequence: 1 aagcgctccaagacacgatt.....ggggttaataaagcgctt 670						
Scoring table: IDENTITY_NUC						
Gapop 10.0 , Gapext 1.0						
Searched: 682709 seqs, 277475446 residues						
Total number of hits satisfying chosen parameters: 718054						
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 65000 summaries						
Database : Issued_Patents_NA:*						
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*						
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*						
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*						
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*						
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*						
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
3076	13.4	2	15	4	US-09-540-824-15	0.893333
c1093	14.4	2.1	17	4	US-09-866-108A-7741	0.847059
c1094	14.4	2.1	17	4	US-09-866-108A-7742	0.847059
3077	13.4	2	16	2	US-08-459-434-6	0.8375
c9064	12.4	1.9	15	1	US-08-142-785-5	0.826667
9065	12.4	1.9	15	1	US-08-142-785-6	0.826667

c9066	12.4	1.9	15	1	US-07-799-824-4	0.826667
c9067	12.4	1.9	15	1	US-07-976-103A-4	0.826667
c9068	12.4	1.9	15	1	US-08-363-240A-665	0.826667
9069	12.4	1.9	15	1	US-08-426-807-1	0.826667
9070	12.4	1.9	15	1	US-08-311-486C-16	0.826667
c9071	12.4	1.9	15	1	US-07-892-902-6	0.826667
9072	12.4	1.9	15	1	US-07-892-902-7	0.826667
c9073	12.4	1.9	15	2	US-08-473-481-4	0.826667
c9074	12.4	1.9	15	2	US-08-585-684B-202	0.826667
9075	12.4	1.9	15	2	US-08-459-434-1	0.826667
c9076	12.4	1.9	15	3	US-09-038-073-202	0.826667
c9077	12.4	1.9	15	3	US-08-338-352-5	0.826667
9078	12.4	1.9	15	4	US-09-202-294-1	0.826667
c9079	12.4	1.9	15	4	US-08-599-738A-4	0.826667
9080	12.4	1.9	15	4	US-09-612-531-4	0.826667
9081	12.4	1.9	15	4	US-09-612-531-8	0.826667
9082	12.4	1.9	15	4	US-09-612-531-9	0.826667
9083	12.4	1.9	15	4	US-09-612-531-10	0.826667
9084	12.4	1.9	15	4	US-09-612-531-14	0.826667
9085	12.4	1.9	15	4	US-09-612-531-15	0.826667
9086	12.4	1.9	15	4	US-09-612-531-16	0.826667
9087	12.4	1.9	15	4	US-09-612-531-17	0.826667
9088	12.4	1.9	15	4	US-09-612-531-18	0.826667
9089	12.4	1.9	15	4	US-09-612-531-19	0.826667
9090	12.4	1.9	15	4	US-09-612-531-20	0.826667
9091	12.4	1.9	15	4	US-09-612-531-21	0.826667
9092	12.4	1.9	15	4	US-09-612-531-22	0.826667
9093	12.4	1.9	15	4	US-09-612-531-23	0.826667
9094	12.4	1.9	15	4	US-09-612-531-24	0.826667
9095	12.4	1.9	15	4	US-09-612-531-25	0.826667
9096	12.4	1.9	15	4	US-09-142-212A-3	0.826667
9097	12.4	1.9	15	4	US-09-142-212A-4	0.826667
9098	12.4	1.9	15	4	US-09-142-212A-5	0.826667
9099	12.4	1.9	15	4	US-09-142-212A-6	0.826667
9100	12.4	1.9	15	4	US-09-142-212A-9	0.826667
9101	12.4	1.9	15	4	US-09-142-212A-13	0.826667
9102	12.4	1.9	15	4	US-09-349-040A-6	0.826667
9103	12.4	1.9	15	4	US-09-349-040A-7	0.826667
9104	12.4	1.9	15	4	US-09-349-040A-8	0.826667
9105	12.4	1.9	15	4	US-09-753-943D-3	0.826667
9106	12.4	1.9	15	4	US-09-753-943D-4	0.826667
9107	12.4	1.9	15	4	US-09-753-943D-6	0.826667
9108	12.4	1.9	15	4	US-09-753-943D-7	0.826667
9109	12.4	1.9	15	4	US-09-753-943D-8	0.826667
9110	12.4	1.9	15	4	US-09-753-943D-9	0.826667
c9111	12.4	1.9	15	4	US-09-753-943D-10	0.826667
c9112	12.4	1.9	15	4	US-09-753-943D-11	0.826667
c9113	12.4	1.9	15	4	US-09-753-943D-12	0.826667
c9114	12.4	1.9	15	4	US-09-753-943D-13	0.826667

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 18:10:30 ; Search time 258.96 Seconds			
(without alignments)			
9632.441 Million cell updates/sec			
Title: US-09-477-082-1			
Perfect score: 670			
Sequence: 1 aagcgctccaagacacgatt.....ggggtaaataaagcgctt 670			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 2458946 seqs, 1861504846 residues			
Total number of hits satisfying chosen parameters: 1244038			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : Published_Applications_NA:*			
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*			
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*			
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*			
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*			
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*			
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*			
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*			
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*			
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*			
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*			
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*			
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*			
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*			
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*			
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*			
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*			
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*			
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*			
Pred. No. is the number of results predicted by chance to have a			
score greater than or equal to the score of the result being printed,			
and is derived by analysis of the total score distribution.			

SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
-----						
4092	13.4	2	15	9	US-09-504-231A-1174	0.893333
4093	13.4	2	15	9	US-09-274-553D-1174	0.893333
c1318	14.4	2.1	17	9	US-09-866-108-7741	0.847059
c1319	14.4	2.1	17	9	US-09-866-108-7742	0.847059
1320	14.4	2.1	17	10	US-09-730-289B-27	0.847059
c1321	14.4	2.1	17	14	US-10-230-006-50	0.847059
c1322	14.4	2.1	17	14	US-10-230-006-547	0.847059
1323	14.4	2.1	17	15	US-10-300-683-252	0.847059
c4094	13.4	2	16	15	US-10-297-068-678	0.8375
690	15	2.2	18	12	US-10-333-429-444	0.833333
12708	12.4	1.9	15	9	US-09-504-231A-1173	0.826667
12709	12.4	1.9	15	9	US-09-274-553D-1173	0.826667
12710	12.4	1.9	15	14	US-10-247-893-4	0.826667
12711	12.4	1.9	15	14	US-10-247-893-8	0.826667
12712	12.4	1.9	15	14	US-10-247-893-9	0.826667
12713	12.4	1.9	15	14	US-10-247-893-10	0.826667
12714	12.4	1.9	15	14	US-10-247-893-14	0.826667
12715	12.4	1.9	15	14	US-10-247-893-15	0.826667
12716	12.4	1.9	15	14	US-10-247-893-16	0.826667
12717	12.4	1.9	15	14	US-10-247-893-17	0.826667
12718	12.4	1.9	15	14	US-10-247-893-18	0.826667
12719	12.4	1.9	15	14	US-10-247-893-19	0.826667
12720	12.4	1.9	15	14	US-10-247-893-20	0.826667
12721	12.4	1.9	15	14	US-10-247-893-21	0.826667
12722	12.4	1.9	15	14	US-10-247-893-22	0.826667
12723	12.4	1.9	15	14	US-10-247-893-23	0.826667
12724	12.4	1.9	15	14	US-10-247-893-24	0.826667
12725	12.4	1.9	15	14	US-10-247-893-25	0.826667
c12726	12.4	1.9	15	14	US-10-024-818-4	0.826667
c12727	12.4	1.9	15	14	US-10-294-203-4	0.826667
c12728	12.4	1.9	15	15	US-10-440-850-111	0.826667
12729	12.4	1.9	15	15	US-10-444-347-28	0.826667
c2046	14	2.1	17	14	US-10-338-777-231	0.823529
c6553	13	1.9	16	15	US-10-297-068-870	0.8125
c2511	13.8	2.1	17	9	US-09-866-108-7743	0.811765
c2512	13.8	2.1	17	9	US-09-866-108-7744	0.811765
c2513	13.8	2.1	17	9	US-09-866-108-9786	0.811765
2514	13.8	2.1	17	9	US-09-866-108-10318	0.811765
2515	13.8	2.1	17	9	US-09-263-959-10	0.811765
2516	13.8	2.1	17	9	US-09-263-959-13	0.811765
c2517	13.8	2.1	17	10	US-09-780-533A-2024	0.811765
c2518	13.8	2.1	17	10	US-09-740-332-1246	0.811765
c2519	13.8	2.1	17	10	US-09-817-879-1246	0.811765

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 16:32:15 ; Search time 2575.47 Seconds			
(without alignments)			
9153.537 Million cell updates/sec			
Title: US-09-477-082-1			
Perfect score: 670			
Sequence: 1 aagcgctccaagacacgatt.....ggggftaaataaagcgctt 670			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 37577330 seqs, 17593059518 residues			
Total number of hits satisfying chosen parameters: 26876998			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : Pending_Patents_NA_Main:*			
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*			
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*			
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*			
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*			
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*			
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*			
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*			
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*			
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*			
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*			
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*			
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*			
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*			
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*			
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*			
16: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*			
17: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*			
18: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*			
19: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*			
20: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*			
21: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*			
22: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*			

23: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*	
24: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*	
25: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*	
26: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*	
27: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*	
28: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*	
29: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*	
30: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*	
31: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*	
32: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*	
33: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*	
34: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*	
35: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*	
36: /cgn2_6/ptodata/2/pna/US098D_COMB.seq:*	
37: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*	
38: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*	
39: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*	
40: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*	
41: /cgn2_6/ptodata/2/pna/US099E_COMB.seq:*	
42: /cgn2_6/ptodata/2/pna/US099F_COMB.seq:*	
43: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*	
44: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*	
45: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*	
46: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*	
47: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*	
48: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*	
49: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*	
50: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*	
51: /cgn2_6/ptodata/2/pna/US104A_COMB.seq:*	
52: /cgn2_6/ptodata/2/pna/US104B_COMB.seq:*	
53: /cgn2_6/ptodata/2/pna/US106_COMB.seq:*	
54: /cgn2_6/ptodata/2/pna/US107A_COMB.seq:*	
55: /cgn2_6/ptodata/2/pna/US107B_COMB.seq:*	
56: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*	
57: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*	
58: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*	
59: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*	
60: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*	
61: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*	
62: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*	
63: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*	
64: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*	
65: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*	
66: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*	
67: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*	
68: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*	
69: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*	
70: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*	
71: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*	
72: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*	
73: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*	

74: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*	
75: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*	
76: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*	
77: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*	
78: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*	
79: /cgn2_6/ptodata/2/pna/US6023A_COMB.seq:*	
80: /cgn2_6/ptodata/2/pna/US6023B_COMB.seq:*	
81: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*	
82: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*	
83: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*	
84: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*	
85: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*	
86: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*	
87: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*	
88: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*	
89: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*	
90: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*	
91: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*	
92: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*	
93: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*	
94: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*	
95: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*	
96: /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*	
97: /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*	
98: /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*	
99: /cgn2_6/ptodata/2/pna/US6042_COMB.seq:*	
100: /cgn2_6/ptodata/2/pna/US6043_COMB.seq:*	
101: /cgn2_6/ptodata/2/pna/US6044_COMB.seq:*	
102: /cgn2_6/ptodata/2/pna/US6045_COMB.seq:*	
103: /cgn2_6/ptodata/2/pna/US6046_COMB.seq:*	
104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:*	
105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:*	
106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:*	
107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:*	
108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:*	
109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:*	
110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
%	
Result	Query
No.	Score Match Length DB ID S/L
-----	
c 667	17 2.5 17 48 US-10-293-338-3956 1
28201	14 2.1 15 5 US-08-168-920E-45 0.933333
16424	14.4 2.1 16 21 US-09-528-209A-1600 0.9
c16425	14.4 2.1 16 48 US-10-287-822-789 0.9

16426	14.4	2.1	16	48	US-10-287-822-790	0.9
c16427	14.4	2.1	16	48	US-10-287-822-791	0.9
c16428	14.4	2.1	16	48	US-10-287-822-4210	0.9
16429	14.4	2.1	16	48	US-10-287-822-4211	0.9
c16430	14.4	2.1	16	48	US-10-287-822A-789	0.9
16431	14.4	2.1	16	48	US-10-287-822A-790	0.9
c16432	14.4	2.1	16	48	US-10-287-822A-791	0.9
c16433	14.4	2.1	16	48	US-10-287-822A-4210	0.9
16434	14.4	2.1	16	48	US-10-287-822A-4211	0.9
c63801	13.4	2	15	1	PCT-US02-25942-3193	0.893333
c63802	13.4	2	15	1	PCT-US02-25942-3705	0.893333
c63803	13.4	2	15	1	PCT-US02-25943-41284	0.893333
63804	13.4	2	15	17	US-09-274-553-2507	0.893333
63805	13.4	2	15	17	US-09-274-553B-1174	0.893333
63806	13.4	2	15	17	US-09-274-553C-1174	0.893333
63807	13.4	2	15	17	US-09-274-553D-1174	0.893333
63808	13.4	2	15	17	US-09-274-553E-1174	0.893333
63809	13.4	2	15	21	US-09-504-231A-1174	0.893333
63810	13.4	2	15	21	US-09-504-231B-1174	0.893333
63811	13.4	2	15	25	US-09-611-931-1174	0.893333
63812	13.4	2	15	25	US-09-611-931A-1174	0.893333
c63813	13.4	2	15	47	US-10-227-565-41284	0.893333
c63814	13.4	2	15	47	US-10-227-567-3193	0.893333
c63815	13.4	2	15	47	US-10-227-567-3705	0.893333
c63816	13.4	2	15	49	US-10-303-778-1347	0.893333
c63817	13.4	2	15	49	US-10-305-274-95	0.893333
c63818	13.4	2	15	49	US-10-305-274-327	0.893333
63819	13.4	2	15	49	US-10-310-188-60805	0.893333
c63820	13.4	2	15	49	US-10-316-958-71	0.893333
c63821	13.4	2	15	50	US-10-367-729A-3193	0.893333
c63822	13.4	2	15	50	US-10-367-729A-3705	0.893333
c63823	13.4	2	15	50	US-10-367-832A-41284	0.893333
7875	15	2.2	17	49	US-10-310-188-60931	0.882353
28202	14	2.1	16	49	US-10-303-778-10272	0.875
c 3	21.8	3.3	25	54	US-10-719-900-746277	0.872
c 4	21.8	3.3	25	99	US-60-427-808-746277	0.872
4786	15.4	2.3	18	49	US-10-310-188-28689	0.855556
16435	14.4	2.1	17	31	US-09-730-289B-27	0.847059
16436	14.4	2.1	17	44	US-10-061-077-79	0.847059
16437	14.4	2.1	17	44	US-10-061-077-80	0.847059
c16438	14.4	2.1	17	47	US-10-230-006-50	0.847059
c16439	14.4	2.1	17	47	US-10-230-006-547	0.847059
16440	14.4	2.1	17	49	US-10-300-683-252	0.847059
16441	14.4	2.1	17	49	US-10-310-188-24680	0.847059
16442	14.4	2.1	17	49	US-10-310-188-60661	0.847059
c16443	14.4	2.1	17	52	US-10-471-271-4464	0.847059
c16444	14.4	2.1	17	52	US-10-471-271-4734	0.847059

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: March 29, 2004, 16:45:00 ; Search time 101.23 Seconds						
(without alignments)						
4020.727 Million cell updates/sec						
Title: US-09-477-082-1						
Perfect score: 670						
Sequence: 1 aagcgctccaagacacgatt.....gggggttaaataaagcgcttt 670						
Scoring table: IDENTITY_NUC						
Gapop 10.0 , Gapext 1.0						
Searched: 1268986 seqs, 303744313 residues						
Total number of hits satisfying chosen parameters: 956702						
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 65000 summaries						
Database : Pending_Patents_NA_New:*						
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*						
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*						
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*						
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*						
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*						
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*						
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result Query						
No.	Score	Match	Length	DB	ID	S/L
-----						
4525	12.8	1.9	16	6	US-10-607-077A-43	0.8
c4526	12.8	1.9	16	6	US-10-708-204-5066	0.8
c 58	15.8	2.4	20	1	PCT-US04-04452-1157	0.79
203	15	2.2	19	5	US-09-646-399A-3	0.789474

16466	11.8	1.8	15	6	US-10-781-758-5	0.786667
16467	11.8	1.8	15	6	US-10-045-674A-622	0.786667
16468	11.8	1.8	15	6	US-10-785-116-5	0.786667
169	15.2	2.3	20	6	US-10-780-439-41	0.76
170	15.2	2.3	20	6	US-10-690-276-106	0.76
171	15.2	2.3	20	6	US-10-690-276-107	0.76
4527	12.8	1.9	17	1	PCT-US03-27118-12	0.752941
59	15.8	2.4	21	1	PCT-US04-00035-9257	0.752381
16469	11.8	1.8	16	6	US-10-776-099-9	0.7375
c16470	11.8	1.8	16	6	US-10-398-483-10	0.7375
119	15.4	2.3	21	6	US-10-470-700A-36	0.733333
2815	13.2	2	18	1	PCT-US04-04452-905	0.733333
7644	12.4	1.9	17	5	US-09-941-492A-16	0.729412
1146	13.8	2.1	19	6	US-10-708-204-4501	0.726316
1147	13.8	2.1	19	6	US-10-664-668-42	0.726316
c1148	13.8	2.1	19	6	US-10-664-668-469	0.726316
1149	13.8	2.1	19	6	US-10-665-951-42	0.726316
c1150	13.8	2.1	19	6	US-10-665-951-469	0.726316
c1151	13.8	2.1	19	6	US-10-444-925A-309	0.726316
c 172	15.2	2.3	21	1	PCT-US04-00035-17210	0.72381
c52331	10.8	1.6	15	1	PCT-US04-07220-7	0.72
c52332	10.8	1.6	15	6	US-10-792-374-28	0.72
2	17.8	2.7	25	7	US-60-545-213-161396	0.712
c4528	12.8	1.9	18	6	US-10-021-698A-6079	0.711111
c 708	14.2	2.1	20	5	US-09-970-851-5	0.71
c12939	12	1.8	17	1	PCT-US03-31862-879	0.705882
12940	12	1.8	17	1	PCT-US03-31862-880	0.705882
12941	12	1.8	17	1	PCT-US03-25614-312	0.705882
12942	12	1.8	17	1	PCT-US03-25614-668	0.705882
c12943	12	1.8	17	6	US-10-488-588-9	0.705882
c 292	14.8	2.2	21	1	PCT-US04-00035-12137	0.704762
c 293	14.8	2.2	21	1	PCT-US04-00035-16634	0.704762
c 294	14.8	2.2	21	1	PCT-US04-00035-17209	0.704762
c 295	14.8	2.2	21	6	US-10-770-726-6140	0.704762
c 296	14.8	2.2	21	6	US-10-770-726-6141	0.704762
c 297	14.8	2.2	21	6	US-10-770-726-6143	0.704762
c 298	14.8	2.2	21	6	US-10-770-726-7109	0.704762
c 299	14.8	2.2	21	6	US-10-770-726-7110	0.704762
300	14.8	2.2	21	6	US-10-786-720-13106	0.704762
904	14	2.1	20	1	PCT-US04-04452-1268	0.7
32789	11.2	1.7	16	6	US-10-796-280-68262	0.7
c 354	14.6	2.2	21	1	PCT-US04-00035-8051	0.695238
355	14.6	2.2	21	1	PCT-US04-00035-54837	0.695238
356	14.6	2.2	21	6	US-10-770-726-3594	0.695238
357	14.6	2.2	21	6	US-10-770-726-8593	0.695238
358	14.6	2.2	21	6	US-10-770-726-8779	0.695238
359	14.6	2.2	21	6	US-10-770-726-9390	0.695238
360	14.6	2.2	21	6	US-10-770-726-18917	0.695238
361	14.6	2.2	21	6	US-10-770-726-18918	0.695238

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 13:22:59 ; Search time 1894.17 Seconds			
(without alignments)			
10562.735 Million cell updates/sec			
Title: US-09-477-082-1			
Perfect score: 670			
Sequence: 1 aagcgctccaagacacgatt.....ggggtaaataaagcgcttt 670			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 27513289 seqs, 14931090276 residues			
Total number of hits satisfying chosen parameters: 78694			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : EST:*			
1: em_estba:*			
2: em_esthum:*			
3: em_estin:*			
4: em_estmu:*			
5: em_estov:*			
6: em_estpl:*			
7: em_estro:*			
8: em_htc:*			
9: gb_est1:*			
10: gb_est2:*			
11: gb_htc:*			
12: gb_est3:*			
13: gb_est4:*			
14: gb_est5:*			
15: em_estfun:*			
16: em_estom:*			
17: em_gss_hum:*			
18: em_gss_inv:*			
19: em_gss_pln:*			
20: em_gss_vrt:*			
21: em_gss_fun:*			
22: em_gss_mam:*			

23: em_gss_mus:*						
24: em_gss_pro:*						
25: em_gss_rod:*						
26: em_gss_phg:*						
27: em_gss_vrl:*						
28: gb_gss1:*						
29: gb_gss2:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
-----						
c7143	11.8	1.8	15	10	BE230585	0.786667
7144	11.8	1.8	15	13	BQ582543	0.786667
7145	11.8	1.8	15	13	BQ585820	0.786667
7146	11.8	1.8	15	13	BQ590410	0.786667
7147	11.8	1.8	15	13	BQ590656	0.786667
7148	11.8	1.8	15	13	BQ591170	0.786667
7149	11.8	1.8	15	13	BQ591178	0.786667
7150	11.8	1.8	15	13	BQ591223	0.786667
7151	11.8	1.8	15	13	BQ594689	0.786667
7152	11.8	1.8	15	14	CF277319	0.786667
7153	11.8	1.8	15	14	CF281923	0.786667
7154	11.8	1.8	15	14	CF290920	0.786667
7155	11.8	1.8	15	14	CF291029	0.786667
7156	11.8	1.8	15	14	CF291103	0.786667
7157	11.8	1.8	15	14	CF291717	0.786667
7158	11.8	1.8	15	14	CF291798	0.786667
7159	11.8	1.8	15	14	CF292458	0.786667
7160	11.8	1.8	15	14	CF292461	0.786667
7161	11.8	1.8	15	14	CF298148	0.786667
7162	11.8	1.8	15	14	CF298630	0.786667
7163	11.8	1.8	15	14	CF298733	0.786667
7164	11.8	1.8	15	14	CF298805	0.786667
7165	11.8	1.8	15	14	CF298889	0.786667
7166	11.8	1.8	15	14	CF299602	0.786667
7167	11.8	1.8	15	14	CF299608	0.786667
7168	11.8	1.8	15	14	CF300121	0.786667
7169	11.8	1.8	15	14	CF300361	0.786667
7170	11.8	1.8	15	14	CF300992	0.786667
7171	11.8	1.8	15	14	CF302034	0.786667
7172	11.8	1.8	15	14	CF302124	0.786667
7173	11.8	1.8	15	14	CF302182	0.786667
7174	11.8	1.8	15	14	CF307923	0.786667

GenCore version 5.1.6				
Copyright (c) 1993 - 2004 Compugen Ltd.				
OM nucleic - nucleic search, using sw model				
Run on: March 29, 2004, 12:49:34 ; Search time 3004.06 Seconds				
(without alignments)				
10864.389 Million cell updates/sec				
Title: US-09-477-082-2				
Perfect score: 753				
Sequence: 1 aattagaccgcgtattgaaa.....tacactgggttttaacctt 753				
Scoring table: IDENTITY_NUC				
Gapop 10.0 , Gapext 1.0				
Searched: 3470272 seqs, 21671516995 residues				
Total number of hits satisfying chosen parameters: 1364278				
Minimum DB seq length: 15				
Maximum DB seq length: 40				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 65000 summaries				
Database : GenEmbl:*				
1: gb_ba:*				
2: gb_htg:*				
3: gb_in:*				
4: gb_om:*				
5: gb_ov:*				
6: gb_pat:*				
7: gb_ph:*				
8: gb_pl:*				
9: gb_pr:*				
10: gb_ro:*				
11: gb_sts:*				
12: gb_sy:*				
13: gb_un:*				
14: gb_vi:*				
15: em_ba:*				
16: em_fun:*				
17: em_hum:*				
18: em_in:*				
19: em_mu:*				
20: em_om:*				
21: em_or:*				
22: em_ov:*				

23: em_pat:*						
24: em_ph:*						
25: em_pl:*						
26: em_ro:*						
27: em_sts:*						
28: em_un:*						
29: em_vi:*						
30: em_htg_hum:*						
31: em_htg_inv:*						
32: em_htg_other:*						
33: em_htg_mus:*						
34: em_htg_pln:*						
35: em_htg_rod:*						
36: em_htg_mam:*						
37: em_htg_vrt:*						
38: em_sy:*						
39: em_htgo_hum:*						
40: em_htgo_mus:*						
41: em_htgo_other:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
-----						
4757	14	1.9	15	6	AR231294	0.933333
c3023	14.4	1.9	16	6	A36563	0.9
3024	14.4	1.9	16	6	AR002257	0.9
3025	14.4	1.9	16	6	AR045207	0.9
3026	14.4	1.9	16	6	AR051238	0.9
c3027	14.4	1.9	16	6	AR087164	0.9
c3028	14.4	1.9	16	6	AR150597	0.9
c3029	14.4	1.9	16	6	E36063	0.9
3030	14.4	1.9	16	6	I16032	0.9
3031	14.4	1.9	16	6	I28367	0.9
c3032	14.4	1.9	16	6	I42181	0.9
c3033	14.4	1.9	16	6	I42187	0.9
c3034	14.4	1.9	16	6	I49619	0.9
c3035	14.4	1.9	16	6	AR200478	0.9
c3036	14.4	1.9	16	6	AR371265	0.9
8238	13.4	1.8	15	6	AR029856	0.893333
c8239	13.4	1.8	15	6	AR029872	0.893333
8240	13.4	1.8	15	6	AR056159	0.893333
8241	13.4	1.8	15	6	AR056160	0.893333

GenCore version 5.1.6					
Copyright (c) 1993 - 2004 Compugen Ltd.					
OM nucleic - nucleic search, using sw model					
Run on: March 29, 2004, 11:54:58 ; Search time 325.436 Seconds					
(without alignments)					
9829.571 Million cell updates/sec					
Title: US-09-477-082-2					
Perfect score: 753					
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753					
Scoring table: IDENTITY_NUC					
Gapop 10.0 , Gapext 1.0					
Searched: 3373863 seqs, 2124099041 residues					
Total number of hits satisfying chosen parameters: 2072792					
Minimum DB seq length: 15					
Maximum DB seq length: 40					
Post-processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 65000 summaries					
Database : N_Geneseq_29Jan04:*					
1: geneseqn1980s:*					
2: geneseqn1990s:*					
3: geneseqn2000s:*					
4: geneseqn2001as:*					
5: geneseqn2001bs:*					
6: geneseqn2002s:*					
7: geneseqn2003as:*					
8: geneseqn2003bs:*					
9: geneseqn2003cs:*					
10: geneseqn2004s:*					
Pred. No. is the number of results predicted by chance to have a					
score greater than or equal to the score of the result being printed,					
and is derived by analysis of the total score distribution.					
SUMMARIES					
%					
Result	Query				
No.	Score	Match	Length	DB	ID S/L
-----					
6	21	2.8	21	3	AAA51822 1
c 7	21	2.8	21	3	AAA51823 1

120	18	2.4	20	9	ADE43355	0.9
3730	14.4	1.9	16	2	AAQ20008	0.9
3731	14.4	1.9	16	2	AAX18362	0.9
10799	13.4	1.8	15	2	AAQ21631	0.893333
10800	13.4	1.8	15	2	AAT00438	0.893333
10801	13.4	1.8	15	2	AAT52140	0.893333
10802	13.4	1.8	15	2	AAT52142	0.893333
10803	13.4	1.8	15	2	AAX14658	0.893333
c10804	13.4	1.8	15	2	AAX14674	0.893333
10805	13.4	1.8	15	5	AAA91455	0.893333
10806	13.4	1.8	15	5	AAA91453	0.893333
c10807	13.4	1.8	15	6	ABK54455	0.893333
10808	13.4	1.8	15	6	ABK81789	0.893333
c10809	13.4	1.8	15	7	ABZ66579	0.893333
c2080	15	2	17	9	ADE25221	0.882353
5799	14	1.9	16	2	AAX61143	0.875
15897	13	1.7	15	3	AAZ59262	0.866667
15898	13	1.7	15	4	AAF81549	0.866667
15899	13	1.7	15	4	AAF49044	0.866667
15900	13	1.7	15	4	AAF49043	0.866667
15901	13	1.7	15	4	AAF49042	0.866667
15902	13	1.7	15	5	AAH23587	0.866667
15903	13	1.7	15	6	ABA97405	0.866667
c15904	13	1.7	15	6	ABK72352	0.866667
15905	13	1.7	15	6	ABK98166	0.866667
15906	13	1.7	15	6	ABK98185	0.866667
15907	13	1.7	15	7	AAD47757	0.866667
15908	13	1.7	15	8	ADB68522	0.866667
8868	13.6	1.8	16	4	AAF82119	0.85
8869	13.6	1.8	16	5	AAH27758	0.85
8870	13.6	1.8	16	6	AAD44149	0.85
126	17.8	2.4	21	3	AAA51818	0.847619
3732	14.4	1.9	17	2	AAQ20006	0.847059
3733	14.4	1.9	17	2	AAQ20005	0.847059
3734	14.4	1.9	17	2	AAX69798	0.847059
3735	14.4	1.9	17	2	AAX69799	0.847059
3736	14.4	1.9	17	4	AAS06654	0.847059
c3737	14.4	1.9	17	7	ACC51390	0.847059
c3738	14.4	1.9	17	7	ACC51389	0.847059
c3739	14.4	1.9	17	7	ABT38540	0.847059
c3740	14.4	1.9	17	7	ADB05248	0.847059
c3741	14.4	1.9	17	7	ADB05249	0.847059
c3742	14.4	1.9	17	9	ADB42730	0.847059
c 324	16.8	2.2	20	7	ABZ77240	0.84
23979	12.6	1.7	15	3	AAA47676	0.84
23980	12.6	1.7	15	6	ABK46570	0.84
c23981	12.6	1.7	15	6	AAD26136	0.84
c23982	12.6	1.7	15	6	ABL91829	0.84
10810	13.4	1.8	16	2	AAT75139	0.8375

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: March 29, 2004, 16:27:20 ; Search time 74.6121 Seconds						
(without alignments)						
5600.675 Million cell updates/sec						
Title: US-09-477-082-2						
Perfect score: 753						
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753						
Scoring table: IDENTITY_NUC						
Gapop 10.0 , Gapext 1.0						
Searched: 682709 seqs, 277475446 residues						
Total number of hits satisfying chosen parameters: 718054						
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 65000 summaries						
Database : Issued_Patents_NA:*						
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*						
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*						
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*						
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*						
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*						
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
2820	14	1.9	15	3	US-08-832-021-28	0.933333
2821	14	1.9	15	4	US-08-275-951-31	0.933333
1801	14.4	1.9	16	1	US-08-087-387-6	0.9
1802	14.4	1.9	16	1	US-08-455-627-6	0.9
c1803	14.4	1.9	16	1	US-08-283-591-16	0.9
c1804	14.4	1.9	16	1	US-08-283-591-25	0.9

c1805	14.4	1.9	16	1	US-08-088-658-34	0.9
1806	14.4	1.9	16	1	US-08-461-271-6	0.9
1807	14.4	1.9	16	1	US-08-713-685A-6	0.9
1808	14.4	1.9	16	2	US-08-689-856-6	0.9
c1809	14.4	1.9	16	2	US-08-471-907A-34	0.9
1810	14.4	1.9	16	3	US-09-070-477-6	0.9
c1811	14.4	1.9	16	3	US-08-088-661F-9	0.9
c1812	14.4	1.9	16	4	US-08-150-156A-21	0.9
c1813	14.4	1.9	16	4	US-08-108-591B-1	0.9
4872	13.4	1.8	15	1	US-08-425-315-1	0.893333
4873	13.4	1.8	15	2	US-08-292-620A-363	0.893333
4874	13.4	1.8	15	2	US-08-292-620A-364	0.893333
4875	13.4	1.8	15	2	US-08-173-489C-45	0.893333
c4876	13.4	1.8	15	2	US-08-173-489C-61	0.893333
4877	13.4	1.8	15	3	US-08-716-190-11	0.893333
4878	13.4	1.8	15	3	US-08-832-021-24	0.893333
4879	13.4	1.8	15	3	US-08-832-021-54	0.893333
4880	13.4	1.8	15	3	US-09-071-845-363	0.893333
4881	13.4	1.8	15	3	US-09-071-845-364	0.893333
2822	14	1.9	16	4	US-09-531-000-9	0.875
7116	13	1.7	15	3	US-08-832-021-25	0.866667
7117	13	1.7	15	3	US-08-832-021-26	0.866667
7118	13	1.7	15	3	US-08-832-021-27	0.866667
1814	14.4	1.9	17	4	US-08-584-040-2548	0.847059
1815	14.4	1.9	17	4	US-08-584-040-2549	0.847059
1816	14.4	1.9	17	4	US-09-371-772B-1072	0.847059
1817	14.4	1.9	17	4	US-09-371-772B-1073	0.847059
4882	13.4	1.8	16	4	US-09-124-238A-4	0.8375
4883	13.4	1.8	16	4	US-09-331-930A-4	0.8375
4884	13.4	1.8	16	4	US-09-721-975-4	0.8375
4885	13.4	1.8	16	4	US-08-894-251A-5	0.8375
4886	13.4	1.8	16	4	US-09-300-958A-56	0.8375
4887	13.4	1.8	16	4	US-09-300-958A-83	0.8375
4888	13.4	1.8	16	4	US-09-986-621-4	0.8375
4889	13.4	1.8	16	4	US-09-527-972-15	0.8375
12749	12.4	1.6	15	1	US-08-087-387-5	0.826667
12750	12.4	1.6	15	1	US-08-455-627-5	0.826667
c12751	12.4	1.6	15	1	US-08-452-196A-6	0.826667
12752	12.4	1.6	15	1	US-07-971-978-1	0.826667
12753	12.4	1.6	15	1	US-08-461-271-5	0.826667
12754	12.4	1.6	15	1	US-08-713-685A-5	0.826667
c12755	12.4	1.6	15	1	US-08-756-728A-2	0.826667
12756	12.4	1.6	15	1	US-08-663-918-3	0.826667
c12757	12.4	1.6	15	1	US-08-663-918-4	0.826667
12758	12.4	1.6	15	2	US-08-689-856-5	0.826667
12759	12.4	1.6	15	2	US-08-292-620A-9	0.826667
12760	12.4	1.6	15	2	US-08-292-620A-360	0.826667
12761	12.4	1.6	15	2	US-08-292-620A-361	0.826667
12762	12.4	1.6	15	2	US-08-292-620A-362	0.826667

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 18:10:30 ; Search time 291.04 Seconds			
(without alignments)			
9632.441 Million cell updates/sec			
Title: US-09-477-082-2			
Perfect score: 753			
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 2458946 seqs, 1861504846 residues			
Total number of hits satisfying chosen parameters: 1244038			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : Published_Applications_NA:*			
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*			
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*			
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*			
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*			
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*			
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*			
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*			
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*			
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*			
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*			
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*			
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*			
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*			
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*			
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*			
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*			
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*			
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*			
Pred. No. is the number of results predicted by chance to have a			
score greater than or equal to the score of the result being printed,			
and is derived by analysis of the total score distribution.			

SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
-----						
2297	14	1.9	15	14	US-10-188-404-31	0.933333
c1457	14.4	1.9	16	9	US-09-955-410-1	0.9
c1458	14.4	1.9	16	9	US-09-983-210-21	0.9
c1459	14.4	1.9	16	14	US-10-154-890-1	0.9
c4547	13.4	1.8	15	14	US-10-157-580A-142	0.893333
c 838	15	2	17	14	US-10-338-777-196	0.882353
7072	13	1.7	15	9	US-09-805-296D-12	0.866667
7073	13	1.7	15	14	US-10-072-975-12	0.866667
7074	13	1.7	15	14	US-10-051-436-12	0.866667
7075	13	1.7	15	15	US-10-360-275-12	0.866667
c 137	16.8	2.2	20	10	US-09-912-724-28	0.84
4548	13.4	1.8	16	9	US-09-811-093-21	0.8375
4549	13.4	1.8	16	9	US-09-777-422-11	0.8375
c4550	13.4	1.8	16	10	US-09-880-313A-42	0.8375
4551	13.4	1.8	16	10	US-09-997-672-30	0.8375
4552	13.4	1.8	16	10	US-09-986-625-4	0.8375
c4553	13.4	1.8	16	10	US-09-894-159-64	0.8375
4554	13.4	1.8	16	10	US-09-854-326-11	0.8375
4555	13.4	1.8	16	12	US-10-362-711-9	0.8375
4556	13.4	1.8	16	14	US-10-136-082-11	0.8375
4557	13.4	1.8	16	14	US-10-163-277-5	0.8375
4558	13.4	1.8	16	14	US-10-136-056-11	0.8375
4559	13.4	1.8	16	14	US-10-261-717-11	0.8375
4560	13.4	1.8	16	14	US-10-284-126-11	0.8375
4561	13.4	1.8	16	14	US-10-283-797-11	0.8375
4562	13.4	1.8	16	14	US-10-283-771-11	0.8375
4563	13.4	1.8	16	14	US-10-261-821-11	0.8375
c4564	13.4	1.8	16	14	US-10-164-915-2	0.8375
4565	13.4	1.8	16	14	US-10-262-258-11	0.8375
4566	13.4	1.8	16	14	US-10-262-264-11	0.8375
4567	13.4	1.8	16	14	US-10-262-252-11	0.8375
4568	13.4	1.8	16	14	US-10-261-787-11	0.8375
4569	13.4	1.8	16	14	US-10-176-812-5	0.8375
4570	13.4	1.8	16	14	US-10-135-671-11	0.8375
4571	13.4	1.8	16	14	US-10-176-549-5	0.8375
4572	13.4	1.8	16	14	US-10-292-951-4	0.8375
4573	13.4	1.8	16	14	US-10-431-304-15	0.8375
4574	13.4	1.8	16	14	US-10-283-874-11	0.8375
4575	13.4	1.8	16	15	US-10-362-262-3	0.8375
c14381	12.4	1.6	15	9	US-09-817-387-22	0.826667
14382	12.4	1.6	15	9	US-09-504-231A-22	0.826667
c14383	12.4	1.6	15	9	US-09-504-231A-1175	0.826667

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 16:32:15 ; Search time 2894.53 Seconds			
(without alignments)			
9153.537 Million cell updates/sec			
Title: US-09-477-082-2			
Perfect score: 753			
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 37577330 seqs, 17593059518 residues			
Total number of hits satisfying chosen parameters: 26876998			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : Pending_Patents_NA_Main:*			
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*			
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*			
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*			
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*			
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*			
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*			
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*			
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*			
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*			
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*			
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*			
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*			
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*			
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*			
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*			
16: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*			
17: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*			
18: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*			
19: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*			
20: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*			
21: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*			
22: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*			

23: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*	
24: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*	
25: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*	
26: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*	
27: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*	
28: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*	
29: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*	
30: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*	
31: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*	
32: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*	
33: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*	
34: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*	
35: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*	
36: /cgn2_6/ptodata/2/pna/US098D_COMB.seq:*	
37: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*	
38: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*	
39: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*	
40: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*	
41: /cgn2_6/ptodata/2/pna/US099E_COMB.seq:*	
42: /cgn2_6/ptodata/2/pna/US099F_COMB.seq:*	
43: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*	
44: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*	
45: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*	
46: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*	
47: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*	
48: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*	
49: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*	
50: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*	
51: /cgn2_6/ptodata/2/pna/US104A_COMB.seq:*	
52: /cgn2_6/ptodata/2/pna/US104B_COMB.seq:*	
53: /cgn2_6/ptodata/2/pna/US106_COMB.seq:*	
54: /cgn2_6/ptodata/2/pna/US107A_COMB.seq:*	
55: /cgn2_6/ptodata/2/pna/US107B_COMB.seq:*	
56: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*	
57: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*	
58: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*	
59: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*	
60: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*	
61: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*	
62: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*	
63: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*	
64: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*	
65: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*	
66: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*	
67: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*	
68: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*	
69: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*	
70: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*	
71: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*	
72: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*	
73: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*	

74:	/cgn2_6/ptodata/2/pna/US6018_COMB.seq:*	
75:	/cgn2_6/ptodata/2/pna/US6019_COMB.seq:*	
76:	/cgn2_6/ptodata/2/pna/US6020_COMB.seq:*	
77:	/cgn2_6/ptodata/2/pna/US6021_COMB.seq:*	
78:	/cgn2_6/ptodata/2/pna/US6022_COMB.seq:*	
79:	/cgn2_6/ptodata/2/pna/US6023A_COMB.seq:*	
80:	/cgn2_6/ptodata/2/pna/US6023B_COMB.seq:*	
81:	/cgn2_6/ptodata/2/pna/US6024_COMB.seq:*	
82:	/cgn2_6/ptodata/2/pna/US6025_COMB.seq:*	
83:	/cgn2_6/ptodata/2/pna/US6026_COMB.seq:*	
84:	/cgn2_6/ptodata/2/pna/US6027_COMB.seq:*	
85:	/cgn2_6/ptodata/2/pna/US6028_COMB.seq:*	
86:	/cgn2_6/ptodata/2/pna/US6029_COMB.seq:*	
87:	/cgn2_6/ptodata/2/pna/US6030_COMB.seq:*	
88:	/cgn2_6/ptodata/2/pna/US6031_COMB.seq:*	
89:	/cgn2_6/ptodata/2/pna/US6032_COMB.seq:*	
90:	/cgn2_6/ptodata/2/pna/US6033_COMB.seq:*	
91:	/cgn2_6/ptodata/2/pna/US6034_COMB.seq:*	
92:	/cgn2_6/ptodata/2/pna/US6035_COMB.seq:*	
93:	/cgn2_6/ptodata/2/pna/US6036_COMB.seq:*	
94:	/cgn2_6/ptodata/2/pna/US6037_COMB.seq:*	
95:	/cgn2_6/ptodata/2/pna/US6038_COMB.seq:*	
96:	/cgn2_6/ptodata/2/pna/US6039_COMB.seq:*	
97:	/cgn2_6/ptodata/2/pna/US6040_COMB.seq:*	
98:	/cgn2_6/ptodata/2/pna/US6041_COMB.seq:*	
99:	/cgn2_6/ptodata/2/pna/US6042_COMB.seq:*	
100:	/cgn2_6/ptodata/2/pna/US6043_COMB.seq:*	
101:	/cgn2_6/ptodata/2/pna/US6044_COMB.seq:*	
102:	/cgn2_6/ptodata/2/pna/US6045_COMB.seq:*	
103:	/cgn2_6/ptodata/2/pna/US6046_COMB.seq:*	
104:	/cgn2_6/ptodata/2/pna/US6047_COMB.seq:*	
105:	/cgn2_6/ptodata/2/pna/US6048_COMB.seq:*	
106:	/cgn2_6/ptodata/2/pna/US6049_COMB.seq:*	
107:	/cgn2_6/ptodata/2/pna/US6050_COMB.seq:*	
108:	/cgn2_6/ptodata/2/pna/US6051_COMB.seq:*	
109:	/cgn2_6/ptodata/2/pna/US6052_COMB.seq:*	
110:	/cgn2_6/ptodata/2/pna/US6053_COMB.seq:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
%		
Result	Query	
No.	Score Match Length DB ID	S/L
-----		
6	21 2.8 21 20	US-09-477-082-33 1
c 7	21 2.8 21 20	US-09-477-082-34 1
c 20	20 2.7 20 48	US-10-293-338-2237 1

c8917	15	2	15	1	PCT-US02-25944-4476	1
c8918	15	2	15	1	PCT-US02-25944-4488	1
c8919	15	2	15	47	US-10-227-564-4476	1
c8920	15	2	15	47	US-10-227-564-4488	1
c2269	16	2.1	17	49	US-10-310-188-24893	0.941176
31751	14	1.9	15	1	PCT-US02-25944-2473	0.933333
31752	14	1.9	15	1	PCT-US02-25944-2498	0.933333
31753	14	1.9	15	46	US-10-188-404-31	0.933333
31754	14	1.9	15	47	US-10-227-564-2473	0.933333
31755	14	1.9	15	47	US-10-227-564-2498	0.933333
c31756	14	1.9	15	49	US-10-305-273-37	0.933333
c31757	14	1.9	15	49	US-10-305-273A-37	0.933333
c31758	14	1.9	15	49	US-10-305-273B-37	0.933333
c 510	17.4	2.3	19	49	US-10-310-188-24640	0.915789
c 511	17.4	2.3	19	49	US-10-310-188-60701	0.915789
c 512	17.4	2.3	19	49	US-10-310-188-72940	0.915789
5273	15.4	2	17	27	US-09-653-225-1416	0.905882
5274	15.4	2	17	54	US-10-712-672-1416	0.905882
270	18	2.4	20	1	PCT-US02-34679-524	0.9
271	18	2.4	20	48	US-10-282-174-524	0.9
272	18	2.4	20	53	US-10-600-009-524	0.9
18606	14.4	1.9	16	1	PCT-US94-07557-6	0.9
18607	14.4	1.9	16	4	US-08-087-386B-6	0.9
18608	14.4	1.9	16	7	US-08-359-295A-10	0.9
c18609	14.4	1.9	16	8	US-08-462-977-1	0.9
c18610	14.4	1.9	16	8	US-08-462-977B-1	0.9
c18611	14.4	1.9	16	8	US-08-468-719-1	0.9
c18612	14.4	1.9	16	8	US-08-468-719A-1	0.9
c18613	14.4	1.9	16	12	US-08-817-067-152	0.9
c18614	14.4	1.9	16	12	US-08-817-067A-152	0.9
c18615	14.4	1.9	16	20	US-09-442-054-34	0.9
c18616	14.4	1.9	16	20	US-09-442-054A-34	0.9
c18617	14.4	1.9	16	40	US-09-955-410-1	0.9
c18618	14.4	1.9	16	42	US-09-983-210-21	0.9
c18619	14.4	1.9	16	46	US-10-154-890-1	0.9
c18620	14.4	1.9	16	48	US-10-287-787-25195	0.9
c2270	16	2.1	18	49	US-10-310-188-83566	0.888889
c8921	15	2	17	49	US-10-310-188-83556	0.882353
c8922	15	2	17	49	US-10-338-777-196	0.882353
c31759	14	1.9	16	49	US-10-303-778-14428	0.875
c31760	14	1.9	16	49	US-10-310-188-26546	0.875
c 513	17.4	2.3	20	48	US-10-293-338-4193	0.87
514	17.4	2.3	20	49	US-10-310-188-1921	0.87
1540	16.4	2.2	19	48	US-10-287-787-25194	0.863158
1541	16.4	2.2	19	49	US-10-310-188-64693	0.863158
5275	15.4	2	18	49	US-10-310-188-9840	0.855556
c5276	15.4	2	18	49	US-10-310-188-14825	0.855556

GenCore version 5.1.6						
Copyright (c) 1993 - 2004 Compugen Ltd.						
OM nucleic - nucleic search, using sw model						
Run on: March 29, 2004, 16:45:00 ; Search time 113.77 Seconds						
(without alignments)						
4020.727 Million cell updates/sec						
Title: US-09-477-082-2						
Perfect score: 753						
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753						
Scoring table: IDENTITY_NUC						
Gapop 10.0 , Gapext 1.0						
Searched: 1268986 seqs, 303744313 residues						
Total number of hits satisfying chosen parameters: 956702						
Minimum DB seq length: 15						
Maximum DB seq length: 40						
Post-processing: Minimum Match 0%						
Maximum Match 100%						
Listing first 65000 summaries						
Database : Pending_Patents_NA_New:*						
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*						
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*						
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*						
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*						
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*						
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*						
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	S/L
28	16.8	2.2	20	6	US-10-690-276-174	0.84
2380	13.4	1.8	16	1	PCT-US04-07616-4	0.8375
8186	12.4	1.6	15	6	US-10-781-758-5	0.826667
8187	12.4	1.6	15	6	US-10-045-674A-622	0.826667
8188	12.4	1.6	15	6	US-10-456-982-8	0.826667

8189	12.4	1.6	15	6	US-10-785-116-5	0.826667
c1329	13.8	1.8	17	1	PCT-US03-25614-376	0.811765
285	15	2	19	6	US-10-708-204-5035	0.789474
17660	11.8	1.6	15	6	US-10-788-232-132	0.786667
8190	12.4	1.6	16	6	US-10-776-099-9	0.775
c8191	12.4	1.6	16	6	US-10-398-483-10	0.775
c 46	16.2	2.2	21	1	PCT-US04-00035-23548	0.771429
c 47	16.2	2.2	21	6	US-10-786-720-6011	0.771429
135	15.4	2	20	6	US-10-667-275A-7	0.77
195	15.2	2	20	1	PCT-US04-04205-2	0.76
196	15.2	2	20	1	PCT-US04-04452-770	0.76
197	15.2	2	20	6	US-10-777-838-2	0.76
198	15.2	2	20	6	US-10-789-113-3	0.76
199	15.2	2	20	6	US-10-789-113-4	0.76
c 200	15.2	2	20	6	US-10-476-021-97	0.76
4842	12.8	1.7	17	6	US-10-398-445-51	0.752941
807	14.2	1.9	19	1	PCT-US03-35072-23	0.747368
808	14.2	1.9	19	6	US-10-387-346B-154	0.747368
c 809	14.2	1.9	19	6	US-10-664-668-173	0.747368
810	14.2	1.9	19	6	US-10-664-668-600	0.747368
c 811	14.2	1.9	19	6	US-10-665-951-173	0.747368
812	14.2	1.9	19	6	US-10-665-951-600	0.747368
c17661	11.8	1.6	16	6	US-10-708-204-4602	0.7375
17662	11.8	1.6	16	6	US-10-647-982A-18	0.7375
c17663	11.8	1.6	16	6	US-10-661-165-203	0.7375
1003	14	1.9	19	6	US-10-664-668-246	0.736842
c1004	14	1.9	19	6	US-10-664-668-673	0.736842
1005	14	1.9	19	6	US-10-665-951-246	0.736842
c1006	14	1.9	19	6	US-10-665-951-673	0.736842
c 136	15.4	2	21	1	PCT-US04-00035-22644	0.733333
c 137	15.4	2	21	1	PCT-US04-00035-23308	0.733333
c 138	15.4	2	21	1	PCT-US04-00035-23309	0.733333
c 139	15.4	2	21	1	PCT-US04-00035-23549	0.733333
c 140	15.4	2	21	1	PCT-US04-00035-23860	0.733333
3128	13.2	1.8	18	6	US-10-653-416-26	0.733333
3129	13.2	1.8	18	6	US-10-785-744-15	0.733333
45580	11	1.5	15	6	US-10-488-619-1683	0.733333
45581	11	1.5	15	6	US-10-641-960-34	0.733333
c8192	12.4	1.6	17	1	PCT-US03-31862-1339	0.729412
8193	12.4	1.6	17	1	PCT-US03-31862-1340	0.729412
8194	12.4	1.6	17	1	PCT-US03-31862-2075	0.729412
c8195	12.4	1.6	17	1	PCT-US03-31862-2076	0.729412
c8196	12.4	1.6	17	1	PCT-US04-06948-25	0.729412
201	15.2	2	21	1	PCT-US04-00035-2986	0.72381
202	15.2	2	21	1	PCT-US04-00035-9540	0.72381
203	15.2	2	21	1	PCT-US04-00035-9756	0.72381
c 204	15.2	2	21	1	PCT-US04-00035-23070	0.72381
205	15.2	2	21	1	PCT-US04-00035-31098	0.72381
206	15.2	2	21	1	PCT-US04-00035-31101	0.72381

GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
OM nucleic - nucleic search, using sw model			
Run on: March 29, 2004, 13:22:59 ; Search time 2128.83 Seconds			
(without alignments)			
10562.735 Million cell updates/sec			
Title: US-09-477-082-2			
Perfect score: 753			
Sequence: 1 aattagaccgcgtattgaaa.....tacactggtttttaacctt 753			
Scoring table: IDENTITY_NUC			
Gapop 10.0 , Gapext 1.0			
Searched: 27513289 seqs, 14931090276 residues			
Total number of hits satisfying chosen parameters: 78694			
Minimum DB seq length: 15			
Maximum DB seq length: 40			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Listing first 65000 summaries			
Database : EST:*			
1: em_estba:*			
2: em_esthum:*			
3: em_estin:*			
4: em_estmu:*			
5: em_estov:*			
6: em_estpl:*			
7: em_estro:*			
8: em_htc:*			
9: gb_est1:*			
10: gb_est2:*			
11: gb_htc:*			
12: gb_est3:*			
13: gb_est4:*			
14: gb_est5:*			
15: em_estfun:*			
16: em_estom:*			
17: em_gss_hum:*			
18: em_gss_inv:*			
19: em_gss_pln:*			
20: em_gss_vrt:*			
21: em_gss_fun:*			
22: em_gss_mam:*			

23: em_gss_mus:*						
24: em_gss_pro:*						
25: em_gss_rod:*						
26: em_gss_phg:*						
27: em_gss_vrl:*						
28: gb_gss1:*						
29: gb_gss2:*						
Pred. No. is the number of results predicted by chance to have a						
score greater than or equal to the score of the result being printed,						
and is derived by analysis of the total score distribution.						
SUMMARIES						
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
-----						
3024	14	1.9	15	10	AW246494	0.933333
c4962	13	1.7	15	14	CF543203	0.866667
c3920	13.4	1.8	16	14	CF291803	0.8375
510	15.8	2.1	19	28	AZ645841	0.831579
96	17.4	2.3	21	28	AZ647578	0.828571
c6707	12.4	1.6	15	10	BE230585	0.826667
6708	12.4	1.6	15	13	BQ582543	0.826667
6709	12.4	1.6	15	13	BQ585820	0.826667
6710	12.4	1.6	15	13	BQ590410	0.826667
6711	12.4	1.6	15	13	BQ590656	0.826667
6712	12.4	1.6	15	13	BQ591170	0.826667
6713	12.4	1.6	15	13	BQ591178	0.826667
6714	12.4	1.6	15	13	BQ591223	0.826667
6715	12.4	1.6	15	13	BQ594689	0.826667
6716	12.4	1.6	15	14	CF277319	0.826667
6717	12.4	1.6	15	14	CF281923	0.826667
c6718	12.4	1.6	15	14	CF290849	0.826667
6719	12.4	1.6	15	14	CF290920	0.826667
6720	12.4	1.6	15	14	CF291029	0.826667
6721	12.4	1.6	15	14	CF291103	0.826667
6722	12.4	1.6	15	14	CF291717	0.826667
6723	12.4	1.6	15	14	CF291798	0.826667
6724	12.4	1.6	15	14	CF292458	0.826667
6725	12.4	1.6	15	14	CF292461	0.826667
6726	12.4	1.6	15	14	CF295100	0.826667
6727	12.4	1.6	15	14	CF296652	0.826667
6728	12.4	1.6	15	14	CF298148	0.826667
6729	12.4	1.6	15	14	CF298630	0.826667
6730	12.4	1.6	15	14	CF298733	0.826667
6731	12.4	1.6	15	14	CF298805	0.826667
6732	12.4	1.6	15	14	CF298889	0.826667
6733	12.4	1.6	15	14	CF299602	0.826667

presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: LICM7 row: D column: 12  
 High quality sequence stop: 14.  
 Location/Qualifiers

## FEATURES

source

```

1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821595"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

## Query Match

1.28; Score 9.2; DB 1; Length 15;

Best local Similarity 78.6%; Pred. No. 0;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 638 TGCCCAAAACAA 651

DB 15 TGATCAAAAAA 2

Search completed: March 31, 2004, 14:14:07  
 Job time : 0.001 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:14:07 ; Search time 0.001 Seconds  
(without alignments)  
22.590 Million cell updates/sec

Title: us094770822

Perfect score: 753  
Sequence: 1 aatgacgcgcgtatgaaa.....tacactgcttttaacctt 753

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 15 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : 2rst.db:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	14	1.9	15 1	AM246494
2	9.2	1.2	15 1	AM246494

## ALIGNMENTS

RESULT 1  
AM246494 15 bp mRNA linear EST 07-JAN-2000  
LOCUS 2821595.3prtime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821595 3'  
DEFINITION mRNA sequence.  
ACCESSION AM246494  
VERSION AM246494.1 GI:6589487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821595.3prtime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing project  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bnlp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

## FEATURES

source

Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 14  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LICM7 row: D column: 12  
High quality sequence stop: 14.  
Location/Qualifiers  
1..15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821595"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOT7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the Laboratory of Gerald W. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.9%; Score 14; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 717 TTTTTCATC 730  
Db 1 TTTTTCATC 14

RESULT 2  
AM246494/c 15 bp mRNA linear EST 07-JAN-2000  
LOCUS 2821595.3prtime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821595 3'  
DEFINITION mRNA sequence.  
ACCESSION AM246494  
VERSION AM246494.1 GI:6589487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821595.3prtime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing project  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bnlp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

```

;
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   PUBLICATION INFORMATION:
;   DOCUMENT NUMBER: WO PCT/EP92/01220
;   FILING DATE: 22-MAY-1992
;   US-09-968-210-21

```

```

Query Match      1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 6.7;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      640 CCGAAGAAACAG 652
DB      4 CCAAAAAAAAAAG 16

```

```

RESULT 7
US-10-154-890-1
; Sequence 1, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter
; APPLICANT: Berg, Rolf Henrik
; TITLE OF INVENTION: Peptide Nucleic Acids
; FILE REFERENCE: ISI50540
; CURRENT APPLICATION NUMBER: US/10/154,890
; PRIOR APPLICATION NUMBER: 2002-05-23
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180734A1 Sequence
US-10-154-890-1

```

```

Query Match      1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 6.7;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      640 CCGAAGAAACAG 652
DB      4 CCAAAAAAAAAAG 16

```

```

RESULT 8
US-10-188-404-31/C
; Sequence 31, Application US/10188404
; Publication No. US20030105286A1
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Nielsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; APPLICANT: Coull, James M.
; APPLICANT: Kieley, John
; APPLICANT: Griffith, Michael
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISI55042
; CURRENT APPLICATION NUMBER: US/10/188,404
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/275,951
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/765,798
; PRIOR FILING DATE: 1997-04-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.1

```

```

; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: misc.feature
; LOCATION: (6)-(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
; OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-31

```

```

Query Match      1.2%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      18 AAGTAAAGAA 29
DB      14 AAGAAAAAAAAA 3

```

```

Search completed: March 31, 2004, 14:11:57
Job time : 0.001 secs

```

```

APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: IS150540
CURRENT APPLICATION NUMBER: US/10/154,890
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/08/108,591
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20030180734A1el Sequence
US-10-154-890-1

```

```

Query Match      1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

CY      715 CTTTTCCTTTTGTGATC 730
DB      16 CTTTTCCTTTTGTGATC 1

```

```

RESULT 4
US-10-188-404-31
Sequence 31, Application US/10188404
Publication No. US20030105286A1
GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Eueholm, Kim L.
APPLICANT: Christensen, Leif
APPLICANT: Coull, James M.
APPLICANT: Griffith, John
APPLICANT: Griffith, Michael
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: IS150542
CURRENT APPLICATION NUMBER: US/10/188,404
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/275,951
PRIOR FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/765,798
PRIOR FILING DATE: 1997-04-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 31
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
FEATURE:
NAME/KEY: misc_feature
LOCATION: (6)..(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-31

```

```

Query Match      1.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

CY      460 CTTTTCCTTTTCTTT 473
DB      2 CTTTTCCTTTTCTTT 15

```

```

RESULT 5
US-09-955-410-1
Sequence 1, Application US/09955410
Patent No. US20020146718A1
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
FILE REFERENCE: IS154800
CURRENT APPLICATION NUMBER: US/09/955,410
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 09/686,114
PRIOR FILING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20020146718A1el Sequence
US-09-955-410-1

```

```

Query Match      1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 6.7;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

CY      640 CCCAAAACACAG 652
DB      4 CCCAAAACACAG 16

```

```

RESULT 6
US-09-983-210-21
Sequence 21, Application US/09983210
Patent No. US20020160383A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN
DIAGNOSTICS AND ANALYTICAL PROCEDURES
NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983,210
FILING DATE: 2001-OCT-23
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150156
FILING DATE: 1994-APR-05
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:11:57 ; Search time 0.001 Seconds  
(without alignments)  
94.878 Million cell updates/sec

Title: us094770822  
Perfect score: 753  
Sequence: 1 aatagaccggtattgaaa.....tacactggttttaccctt 753

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 63 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : 2rnpb.db:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	14.4	1.9	16	1	US-09-955-410-1
C 2	14.4	1.9	16	1	US-09-983-210-21
C 3	14.4	1.9	16	1	US-10-154-890-1
C 4	14.4	1.9	15	1	US-10-188-404-31
C 5	9.8	1.3	16	1	US-09-955-410-1
C 6	9.8	1.3	16	1	US-09-983-210-21
C 7	9.8	1.3	16	1	US-10-154-890-1
C 8	8.8	1.2	15	1	US-10-188-404-31

## ALIGNMENTS

RESULT 1  
US-09-955-410-1/c  
; Sequence 1, Application US/09955410  
; Patent No. US20020146718A1  
; GENERAL INFORMATION:  
; APPLICANT: Buchardt, Ole  
; APPLICANT: Escholtz, Michael  
; APPLICANT: Nielsen, Peter Eigil  
; APPLICANT: Berg, Rolf Henrik  
; TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases  
; FILE REFERENCE: IS184800  
; CURRENT APPLICATION NUMBER: US/09/955,410  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: 08/108,591  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR APPLICATION NUMBER: 09/586,114  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1

LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20020146718A1 Sequence  
US-09-955-410-1

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.2;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 715 CTTTCTTTTTCATC 730  
Db 16 CTTTCTTTTTCATC 1

RESULT 2  
US-09-983-210-21/c  
; Sequence 21, Application US/09983210  
; Patent No. US20020160383A1  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN  
; TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES  
; NUMBER OF SEQUENCES: 40  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/983,210  
; FILING DATE: 2001-OCT-23  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150156  
; FILING DATE: 1994-APR-05  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0986/91  
; FILING DATE: 24-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0987/91  
; FILING DATE: 24-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0510/92  
; FILING DATE: 15-APR-1992  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; DOCUMENT NUMBER: WO PCT/EP92/01220  
; FILING DATE: 22-MAY-1992  
US-09-983-210-21

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 1.2;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 715 CTTTCTTTTTCATC 730  
Db 16 CTTTCTTTTTCATC 1

RESULT 3  
US-10-154-890-1/c  
; Sequence 1, Application US/10154890  
; Publication No. US20030180734A1  
; GENERAL INFORMATION:

```
TOPOLOGY: linear
US-09-070-477-6

Query Match      1.2%; Score 9.4; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      643 AAAAAACAGT 653
      |||||
Db      11 AAAAAAAGT 1

RESULT 29
US-08-275-951-31/c
; Sequence 31, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kieley, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coul, James M.
; APPLICANT: Neilson, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS1577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968e1 Sequence
; NAME/KEY: misc_feature
; LOCATION: (6)..(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
; OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-31

Query Match      1.2%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      18 AAGTAAAGAA 29
      |||||
Db      14 AAGAAAAAAA 3

RESULT 30
US-08-832-021-28/c
; Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
```

```
APPLICANT: Parimoo, S.
APPLICANT: Proutty, S.
APPLICANT: Steen, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: USP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

Query Match      1.1%; Score 8.4; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      642 CAATAACAA 651
      |||||
Db      13 CAATAACAA 4

Search completed: March 31, 2004, 14:10:54
Job time : 0.001 secs
```

```

/ APPLICANT: Sergei M. Gryaznov
/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
/ TITLE OF INVENTION: and therapeutic applications
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
/ STREET: 465 Lincoln Centre Drive
/ CITY: Foster City
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94044
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: Windows 3.1/DOS 5.0
/ SOFTWARE: Microsoft Word for Windows, vers. 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/713,685A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/461,271
/ FILING DATE:
/ APPLICATION NUMBER: 08/087,387
/ FILING DATE: 2-Jul-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stephen C. Macevicz
/ REGISTRATION NUMBER: 30,285
/ REFERENCE/DOCKET NUMBER: 104
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 358-7855
/ TELEFAX: (415) 358-7794
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-713-685A-6
/
Query Match 1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity 90.3%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAAAGT 653
DB 11 AAAAAAAGT 1

RESULT 27
US-08-689-856-6/c
/ Sequence 6, Application US/08689856
/ Patent No. 5830658
/ GENERAL INFORMATION:
/ APPLICANT: Sergei M. Gryaznov
/ TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
/ TITLE OF INVENTION: Connected Macromolecular Structures
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooley Godward LLP
/ STREET: Five Palo Alto Square, 3000 El Camino Real
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94306-2155
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/689,856
/ FILING DATE:

```

```

/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/455,627
/ FILING DATE: 31-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nakamura, Jackie N.
/ REGISTRATION NUMBER: 35,966
/ REFERENCE/DOCKET NUMBER: LYNX-003/01 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-843-5000
/ TELEFAX: 415-857-0663
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-689-856-6
/
Query Match 1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAAAGT 653
DB 11 AAAAAAAGT 1

RESULT 28
US-09-070-477-6/c
/ Sequence 6, Application US/09070477
/ Patent No. 6048974
/ GENERAL INFORMATION:
/ APPLICANT: Sergei M. Gryaznov
/ TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
/ TITLE OF INVENTION: and therapeutic applications
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
/ STREET: 465 Lincoln Centre Drive
/ CITY: Foster City
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: Windows 3.1/DOS 5.0
/ SOFTWARE: Microsoft Word for Windows, vers. 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/070,477
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/713,685
/ FILING DATE: 08/461,271
/ APPLICATION NUMBER: 08/087,387
/ FILING DATE: 2-Jul-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stephen C. Macevicz
/ REGISTRATION NUMBER: 30,285
/ REFERENCE/DOCKET NUMBER: 104
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 358-7794
/ TELEFAX: (415) 358-7855
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single

```

STATE: California  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,387  
FILING DATE: 19930702  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevitz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 358-7855  
TELEFAX: (415) 358-7794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-087-387-6

Query Match 1.2%; Score 9.4; DB 1; Length 16;  
Best Local Similarity 90.9%; Pred. No. 26;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAACACT 653  
DB 11 AAAAAAAAGT 1

RESULT 24  
US-08-455-627-6/C  
Sequence 6, Application US/08455627  
Patent No. 5571677  
GENERAL INFORMATION:  
APPLICANT: Sergei M. Gryaznov  
TITLE OF INVENTION: Convenient Synthesis of Branched and Multiply  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Cooley Godward LLP  
STREET: Five Palo Alto Square, 3000 El Camino Real  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,627  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N.  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:

LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-627-6

Query Match 1.2%; Score 9.4; DB 1; Length 16;  
Best Local Similarity 90.9%; Pred. No. 26;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAACACT 653  
DB 11 AAAAAAAAGT 1

RESULT 25  
US-08-461-271-6/C  
Sequence 6, Application US/08461271  
Patent No. 5741643  
GENERAL INFORMATION:  
APPLICANT: Sergei M. Gryaznov  
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Stephen C. Macevitz, Lynx Therapeutics  
STREET: 465 Lincoln Centre Drive  
CITY: Foster City  
STATE: California  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,271  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/087,387  
FILING DATE: 2-JUL-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevitz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 358-7855  
TELEFAX: (415) 358-7794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-461-271-6

Query Match 1.2%; Score 9.4; DB 1; Length 16;  
Best Local Similarity 90.9%; Pred. No. 26;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAACACT 653  
DB 11 AAAAAAAAGT 1

RESULT 26  
US-08-713-685A-6/C  
Sequence 6, Application US/08713685A  
Patent No. 5817795  
GENERAL INFORMATION:

LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-471-907A-34

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
Db 4 CCAAAAACAG 16

RESULT 20  
US-08-088-661F-9  
Sequence 9, Application US/08088661F  
Patent No. 6228982  
GENERAL INFORMATION:  
APPLICANT: No. 6228982den, Bengert  
APPLICANT: Wiltung, Pernilla  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf  
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids  
FILE REFERENCE: ISTS1108  
CURRENT APPLICATION NUMBER: US/08/088,661F  
CURRENT FILING DATE: 1993-07-02  
PRIOR APPLICATION NUMBER: 08/054,363  
PRIOR FILING DATE: 1993-04-26  
PRIOR APPLICATION NUMBER: PCT/EP92/01219  
PRIOR FILING DATE: 1992-05-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence  
US-08-088-661F-9

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
Db 4 CCAAAAACAG 16

RESULT 21  
US-08-150-156A-21  
Sequence 21, Application US/08150156A  
Patent No. 6357163  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN  
TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES  
NUMBER OF SEQUENCES: 40  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/150,156A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0986/91  
FILING DATE: 24-MAY-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0987/91  
FILING DATE: 24-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0510/92  
FILING DATE: 15-APR-1992  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO PCT/EP92/01220  
FILING DATE: 22-MAY-1992  
US-08-150-156A-21

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
Db 4 CCAAAAACAG 16

RESULT 22  
US-08-108-591B-1  
Sequence 1, Application US/08108591B  
Patent No. 6395474  
GENERAL INFORMATION:  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter Elgil  
APPLICANT: Berg, Rolf Henrik  
TITLE OF INVENTION: Peptide Nucleic Acids  
FILE REFERENCE: ISTS0540  
CURRENT APPLICATION NUMBER: US/08/108,591B  
CURRENT FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: No. 6395474el Sequence  
US-08-108-591B-1

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
Db 4 CCAAAAACAG 16

RESULT 23  
US-08-087-387-6/c  
Sequence 6, Application US/08087387  
Patent No. 5473060  
GENERAL INFORMATION:  
APPLICANT: Sergei M. GYAZNOV  
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Stephen C. Macevicz, Lynx Therapeutics  
STREET: 465 Lincoln Centre Drive  
CITY: Foster City

TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND  
TITLE OF INVENTION: OLIGO -LACTAMAMIDES  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
ADDRESSEE: No. 5629152rls  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,591  
FILING DATE: N/A  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-283-591-25

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 640 CCAAAAACAG 652  
DB 4 CCAAAAACAG 16

RESULT 18  
US-08-088-658-34  
Sequence 34, Application US/08088658  
Patent No. 5641625  
GENERAL INFORMATION:  
APPLICANT: Ecker, David J.  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf H.  
APPLICANT: M Ilegard, Niels E.  
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE  
TITLE OF INVENTION: NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625rls  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/088,658  
FILING DATE: 19930702  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: 08/054,363  
APPLICATION NUMBER: 08/054,363  
FILING DATE: 26-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lucci, Joseph  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-1052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-088-658-34

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
Best Local Similarity 84.6%; Pred. No. 25;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 640 CCAAAAACAG 652  
DB 4 CCAAAAACAG 16

RESULT 19  
US-08-471-907A-34  
Sequence 34, Application US/08471907A  
Patent No. 5986053  
GENERAL INFORMATION:  
APPLICANT: Ecker, David J.  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf H.  
APPLICANT: M Ilegard, Niels E.  
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE  
TITLE OF INVENTION: NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053rls  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,907A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/088,658  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lucci, Joseph  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: ISIS-1052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:

```

RESULT 14
US-08-832-021-28
; Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Paridinas, J.
; APPLICANT: Parimoc, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

```

```

Query Match      1.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      716 TTTTTCCTTTTGGAT 729
Db      2 TTTTTCCTTTTGGAT 15

```

```

RESULT 15
US-08-275-951-31
; Sequence 31, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Echolm, Michael
; APPLICANT: Kieley, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dusholtz, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: IS151577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
; NAME/KEY: misc_feature

```

```

; LOCATION: (6)..(7)
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
; OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
US-08-275-951-31

```

```

Query Match      1.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      460 CTTTTCCTTTTCTTT 473
Db      2 CTTTTCCTTTTCTTT 15

```

```

RESULT 16
US-08-283-591-16
; Sequence 16, Application US/08283591
; Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga
; TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND
; TITLE OF INVENTION: OLIGO -LACTAMAMIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSER: No. 5629152118
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,591
; FILING DATE: N/A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-283-591-16

Query Match      1.3%; Score 9.8; DB 1; Length 16;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      640 CCCAAAAAAGAG 652
Db      4 CCAAAAAAAGAG 16

RESULT 17
US-08-283-591-25
; Sequence 25, Application US/08283591
; Patent No. 5629152
; GENERAL INFORMATION:
; APPLICANT: Ravikumar, Vasulinga

```

FILING DATE:  
APPLICATION NUMBER: 08/087,387  
FILING DATE: 2-Jul-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevitz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 358-7855  
TELEFAX: (415) 358-7794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-070-477-6

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTCTTTCTTTT 474  
DB 1 ACTTTTCTTTCTTTT 16

RESULT 11  
US-08-086-661F-9/C  
Sequence 9, Application US/08086661F  
Patent No. 6228982  
GENERAL INFORMATION:  
APPLICANT: No. 6228982den, Bengel  
APPLICANT: Wiltung, Pernilla  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf  
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids  
FILE REFERENCE: IS15108  
CURRENT APPLICATION NUMBER: US/08/086,661F  
CURRENT FILING DATE: 1993-07-02  
PRIOR APPLICATION NUMBER: 06/054,363  
PRIOR FILING DATE: 1993-04-26  
PRIOR APPLICATION NUMBER: PCT/EP92/01219  
PRIOR FILING DATE: 1992-05-19  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence  
US-08-086-661F-9

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGGATC 730  
DB 16 CTTTTTTTGGATC 1

RESULT 12  
US-08-150-156A-21/C  
Sequence 21, Application US/08150156A  
Patent No. 6357163  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN  
TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES

NUMBER OF SEQUENCES: 40  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/150,156A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0986/91  
FILING DATE: 24-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0987/91  
FILING DATE: 24-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 0510/92  
FILING DATE: 15-APR-1992  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: NO PCT/EP92/01220  
FILING DATE: 22-MAY-1992  
US-08-150-156A-21

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGGATC 730  
DB 16 CTTTTTTTGGATC 1

RESULT 13  
US-08-108-591B-1/C  
Sequence 1, Application US/08108591B  
Patent No. 6395474  
GENERAL INFORMATION:  
APPLICANT: Buchardt, Ole  
APPLICANT: Egholm, Michael  
APPLICANT: Nielsen, Peter Eghil  
APPLICANT: Berg, Rolf Henrik  
TITLE OF INVENTION: Peptide Nucleic Acids  
FILE REFERENCE: IS150540  
CURRENT APPLICATION NUMBER: US/08/108,591B  
CURRENT FILING DATE: 2001-08-13  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: No. 6395474el Sequence  
US-08-108-591B-1

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGGATC 730  
DB 16 CTTTTTTTGGATC 1

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTCTTTT 474

Db 1 ACTTTTCTTTT 16

## RESULT 8

US-08-689-856-6

Sequence 6, Application US/08689856

Patent No. 5830658

GENERAL INFORMATION:

APPLICANT: Sergei M. Gryaznov

TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply

TITLE OF INVENTION: Connected Macromolecular Structures

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward LLP

STREET: Five Palo Alto Square, 3000 El Camino Real

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/689,856

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/455,627

FILING DATE: 31-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Nakamura, Jackie N.

REGISTRATION NUMBER: 35,966

REFERENCE/DOCKET NUMBER: LYNX-003/01 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-843-5000

TELEFAX: 415-857-0663

INFORMATION FOR SEQ. ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-689-856-6

Query Match

Best Local Similarity 1.9%; Score 14.4; DB 1; Length 16;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTCTTTT 474

Db 1 ACTTTTCTTTT 16

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053-11

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,907A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/088,658

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lucchi, Joseph

REGISTRATION NUMBER: 33,307

REFERENCE/DOCKET NUMBER: ISIS-1052

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ. ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 16

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-471-907A-34

Query Match

Best Local Similarity 1.9%; Score 14.4; DB 1; Length 16;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGTATC 730

Db 16 CTTTTTTTGTATC 1

## RESULT 10

US-09-070-477-6

Sequence 6, Application US/09070477

Patent No. 6048974

GENERAL INFORMATION:

APPLICANT: Sergei M. Gryaznov

TITLE OF INVENTION: Oligonucleotide clamps having diagnostic

TITLE OF INVENTION: and therapeutic applications

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics

STREET: 465 Lincoln Centre Drive

CITY: Foster City

STATE: California

COUNTRY: USA

ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows 3.1/DOS 5.0

SOFTWARE: Microsoft Word for Windows, vers. 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,477

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/713,685

FILING DATE:

APPLICATION NUMBER: 08/461,271

APPLICANT: M liegaard, Niels E.  
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE  
TITLE OF INVENTION: NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz and No. 5641625r1s  
STREET: One liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/089,658  
FILING DATE: 19930702  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,363  
FILING DATE: 26-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Lucet, Joseph  
REGISTRATION NUMBER: 33,307  
REFERENCE/DOCKET NUMBER: 1SIS-1052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-088-658-34

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTTTGATC 730  
DB 16 CTTTTTTTTTGATC 1

RESULT 6  
US-08-461-271-6  
Sequence 6, Application US/08461271  
Patent No. 5741643  
GENERAL INFORMATION:  
APPLICANT: Sergei M. Gryaznov  
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
TITLE OF INVENTION: and therapeutic applications  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Stephen C. Macevicz, Lynx Therapeutics  
STREET: 465 Lincoln Centre Drive  
CITY: Foster City  
STATE: California  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,271  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/087,387  
FILING DATE: 2-Jul-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevicz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 358-7855  
TELEFAX: (415) 358-7794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-461-271-6

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTTTCTTTT 474  
DB 1 ACTTTTTTCTTTT 16

RESULT 7  
US-08-713-685A-6  
Sequence 6, Application US/0873685A  
Patent No. 581795  
GENERAL INFORMATION:  
APPLICANT: Sergei M. Gryaznov  
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic  
TITLE OF INVENTION: and therapeutic applications  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Stephen C. Macevicz, Lynx Therapeutics  
STREET: 465 Lincoln Centre Drive  
CITY: Foster City  
STATE: California  
COUNTRY: USA  
ZIP: 94404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,685A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/461,271  
FILING DATE:  
APPLICATION NUMBER: 08/087,387  
FILING DATE: 2-Jul-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevicz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 358-7855  
TELEFAX: (415) 358-7794  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-713-685A-6

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,627  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Jackie N.  
REGISTRATION NUMBER: 35,966  
REFERENCE/DOCKET NUMBER: LYNX-003/01 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-455-627-6

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTTCCTTTT 474  
DB 1 ACTTTTTCCTTTT 16

RESULT 3  
US-08-283-591-16/c  
Sequence 16, Application US/08283591  
Patent No. 5629152

GENERAL INFORMATION:  
APPLICANT: Ravikumar, Vasulinga  
TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,591  
FILING DATE: N/A  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-283-591-16

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 715 CTTTTCCTTTTGATC 730  
DB 16 CTTTTCCTTTTGATC 1

RESULT 4  
US-08-283-591-25/c  
Sequence 25, Application US/08283591  
Patent No. 5629152

GENERAL INFORMATION:  
APPLICANT: Ravikumar, Vasulinga  
TITLE OF INVENTION: NOVEL TRISUBSTITUTED -LACTAMS AND  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/283,591  
FILING DATE: N/A  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME:  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-283-591-25

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTCCTTTTGATC 730  
DB 16 CTTTTCCTTTTGATC 1

RESULT 5  
US-08-088-658-34/c  
Sequence 34, Application US/08088658  
Patent No. 5641625

GENERAL INFORMATION:  
APPLICANT: Ecker, David J.  
APPLICANT: Buchardt, Ole  
APPLICANT: Egnolm, Michael  
APPLICANT: Nielsen, Peter E.  
APPLICANT: Berg, Rolf H.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:10:54 ; Search time 0.001 Seconds  
(without alignments)  
358.428 Million cell updates/sec

Title: us094770822

Perfect score: 753

Sequence: 1 aactagacgcgtattgaa.....tactcgttttttaacctt 753

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 15 segs, 238 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: 2rmi.db:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	14.4	1.9	16	1	US-08-087-387-6
2	14.4	1.9	16	1	US-08-455-627-6
3	14.4	1.9	16	1	US-08-283-591-16
4	14.4	1.9	16	1	US-08-283-591-25
5	14.4	1.9	16	1	US-08-088-658-34
6	14.4	1.9	16	1	US-08-461-271-6
7	14.4	1.9	16	1	US-08-713-685A-6
8	14.4	1.9	16	1	US-08-689-856-6
9	14.4	1.9	16	1	US-08-471-907A-34
10	14.4	1.9	16	1	US-09-070-477-6
11	14.4	1.9	16	1	US-08-088-661F-9
12	14.4	1.9	16	1	US-08-150-156A-21
13	14.4	1.9	16	1	US-08-108-591B-1
14	14.4	1.9	15	1	US-08-832-021-28
15	14.4	1.9	15	1	US-08-275-951-31
16	14.4	1.9	16	1	US-08-283-591-16
17	9.8	1.3	16	1	US-08-088-658-34
18	9.8	1.3	16	1	US-08-088-658-34
19	9.8	1.3	16	1	US-08-471-907A-34
20	9.8	1.3	16	1	US-08-088-661F-9
21	9.8	1.3	16	1	US-08-150-156A-21
22	9.8	1.3	16	1	US-08-108-591B-1
23	9.4	1.2	16	1	US-08-087-387-6
24	9.4	1.2	16	1	US-08-455-627-6
25	9.4	1.2	16	1	US-08-461-271-6
26	9.4	1.2	16	1	US-08-713-685A-6
27	9.4	1.2	16	1	US-08-689-856-6
28	9.4	1.2	16	1	US-09-070-477-6
29	8.8	1.1	15	1	US-08-275-951-31
30	8.4	1.1	15	1	US-08-832-021-28

## ALIGNMENTS

```
RESULT 1
US-08-087-387-6
; Sequence 6, Application US/08087387
; Patent No. 5473060
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Oligonucleotide clamps having diagnostic and therapeutic applic
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Stephen C. Macevitz, Lynx Therapeutics
; STREET: 465 Lincoln Centre Drive
; CITY: Foster City
; STATE: California
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch diskette
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,387
; FILING DATE: 19930702
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen C. Macevitz
; REGISTRATION NUMBER: 30,285
; REFERENCE/DOCKET NUMBER: 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-7855
; TELEFAX: (415) 358-7794
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-087-387-6

Query Match          1.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 4.3;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTTCCTTTT 474
Db 1 ACTTTTTCCTTTT 16

RESULT 2
US-08-455-627-6
; Sequence 6, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```

XX 31-OCT-2000 (first entry)
DT Antisense primer for untreated CASP8 wild type DNA.
DE
XX
DE CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
XX tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
XX death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
XX MO200039347-A1.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031280.
XX
XX 31-DEC-1998; 98US-0114308P.
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Kidd VJ, Lahti JM, Teitz T;
XX
XX WPI; 2000-452423/39.
XX
XX
XX Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or
PT prognosing cancer; comprises detecting a modification of genomic DNA
PT comprising the CASP8 gene that results in inactivation of the gene.
XX
XX Example 3; Page 61; 107pp; English.
XX
XX Investigation of silencing of caspase-8 (CASP8) gene by methylation was
CC analyzed using methylation-sensitive PCR analysis. Amplification of the
CC 5' untranslated region (UTR) of the Casp8 gene was performed in reaction
CC mixtures containing bisulfite treated DNA. Primers AA51818-23 were
CC designed to produce a 320 bp fragment in the upstream region of Casp8
CC gene extending from nucleotides +221 to +541. Wild type primers were used
CC to amplify the corresponding region of untreated genomic DNA. Controls
CC without DNA were also performed. CASP8, a cysteine protease, is part of
CC the death inducing signaling complex (DISC) associated with the Fas
CC receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
CC suppressor gene. The CASP8 promoter region sequences, in particular
CC Region 1 and Region 2, are crucial to the design and execution of the
CC genomic methylation PCR analysis of CASP8 gene inactivation. Methylation
CC PCR can be used to examine even minute amounts of patient material to
CC demonstrate whether the CASP8 gene expresses an mRNA and protein product.
CC The CASP8 gene has been localized to human chromosome 2q33-34. The
CC methods are used to diagnose or prognose cancer. Cancer is treated by
CC administering a vector that expresses a gene encoding functional CASP8 in
CC cells. The cancer that is diagnosed or treated is a tumour in which a myc
CC gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,
CC juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-
CC cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma
CC can be diagnosed with the new method. A kit for screening for a compound
CC that induces death-receptor-mediated apoptosis in cells containing an
CC inactivated CASP8 gene is also provided
XX
XX
SQ Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.2%; Score 9.2; DB 1; Length 21;
XX Best Local Similarity 78.6%; Pred. No. 7.3;
XX Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 670 ATGTGATTCGCGG 683
XX | | | | | | | | | |
XX Db 6 ATCTGATTCGAGG 19
XX
XX
XX RESULT 10
XX ADE43355/c
XX ID ADE43355 standard; DNA; 20 BP.
XX
XX ADE43355;

```

```

XX 29-JAN-2004 (first entry)
DT Human uPA primer, SEQ ID 524.
DE
XX
DE Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6;
XX Alzheimer's disease; neuroprotective; neurotrophic; gene therapy;
XX Chromosome 10; PCR; primer; ss.
XX
XX
XX Homo sapiens.
XX
XX MO2003054143-A2.
XX
XX 03-JUL-2003.
XX
XX 25-OCT-2002; 2002WO-US034679.
XX
XX 25-OCT-2001; 2001US-0339522P.
XX
XX 08-NOV-2001; 2001US-0336929P.
XX
XX 08-NOV-2001; 2001US-0338010P.
XX
XX 09-NOV-2001; 2001US-0338363P.
XX
XX 04-DEC-2001; 2001US-0337052P.
XX
XX 28-MAR-2002; 2002US-0368919P.
XX
XX (NEUR-) NEUROGENETICS INC.
XX (GENO) GEN HOSPITAL CORP.
XX
XX Becker KD, Velicelebi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;
XX Saunders AJ, Mullin KM, Sampson AJ, Blacker D;
XX
XX WPI; 2003-559131/52.
XX
XX
XX Determining a predisposition for or the occurrence of neurodegenerative
PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid
PT the presence or absence of an allelic variant of one or more polymorphic
PT regions.
XX
XX Example 4; Page 313; 848pp; English.
XX
XX
XX The present invention relates to a method (M1) for determining a
CC predisposition for or the occurrence of neurodegenerative disease in a
CC subject. The method comprises detecting in a target nucleic acid obtained
CC from the subject the presence or absence of an allelic variant of one or
CC more polymorphic regions of one or more genes selected from uPA
CC (urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulin-
CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid
CC lipase), and TNFRSF6 (tumour necrosis factor receptor-56), where the
CC presence of at least one of the allelic variant of one or more
CC polymorphic regions is indicative of a predisposition for or the
CC occurrence of neurodegenerative disease. The genes are all located on
CC chromosome 10. M1 is useful for determining a predisposition for or the
CC occurrence of, and for treating neurodegenerative disease, particularly
CC Alzheimer's disease. The present sequence is a PCR primer, which was used
CC in the method of the invention.
XX
XX
SQ Sequence 20 BP; 1 A; 12 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 1.1%; Score 8.6; DB 1; Length 20;
XX Best Local Similarity 73.3%; Pred. No. 8.1;
XX Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 208 ACAGGCGCTGTGGCGG 222
XX | | | | | | | | | |
XX Db 19 AGAGGCGCAGGAGCGG 5
XX
XX
XX Search completed: March 31, 2004, 14:10:08
XX
XX Job time : 0.001 secs

```

PCR can be used to examine even minute amounts of patient material to demonstrate whether the CASP8 gene expresses an mRNA and protein product. The CASP8 gene has been localized to human chromosome 2q33-34. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated apoptosis in cells containing an inactivated CASP8 gene is also provided

Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.5%; Score 11.6; DB 1; Length 21;  
Best Local Similarity 77.8%; Pred. No. 5.1;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

340 GCAGTCTCCAGTCCCTCT 357  
19 GCAGTCTCCAGTCCCTCT 2

## RESULT 7

AAQ20008/c  
ID AAQ20008 standard; DNA; 16 BP.

AAQ20008;

01-APR-1992 (first entry)

Oligonucleotide #4 able to covalently cross-link to target DNA.

deoxyribonucleic acid; major groove; ethanocamino group;  
aziridinylcytosine; cross-linking group; ss.

Synthetic.

Key Location/Qualifiers  
modified\_base 8  
/\*tag= a  
/mod\_base= OTHER  
/note= "N4-ethanocytosine"

modified\_base 14  
/\*tag= b  
/mod\_base= msc

W09118997-A.

12-DEC-1991.

25-MAY-1990;

25-MAY-1990; 90US-00529346.

25-MAY-1990; 90US-00529346.

14-JAN-1991; 91US-00640654.

(GILE-) GILEAD SCIB INC.

Mattewcci MD, Krawczyk S;

WPI; 1992-007480/01.

New sequence-specific non-photo-activated crosslinking agents - bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. HIV.

Example 2; Page 21; 42pp; English.

The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is one of four oligonucleotides which were designed to specifically bind and cross-link to the duplex target sequence AAQ20004. Oligo #4 with its internal cross-linking group was less effective than the other

oligonucleotides with terminal cross-linking groups. See also AAQ20005-7

Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.4%; Score 10.4; DB 1; Length 16;  
Best Local Similarity 91.7%; Pred. No. 8.2;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

19 AAGTAAAGAAA 30

16 AAGAAAGAAA 5

## RESULT 8

AA18362/c  
ID AA18362 standard; DNA; 16 BP.

AA18362;

11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 3.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
Synthetic.

JP11032765-A.

09-FEB-1999.

18-JUL-1997; 97JP-00208312.

18-JUL-1997; 97JP-00208312.

(TAKI) TAKARA SHUZO CO LTD.

WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in RT-PCR.

Peptides having at least two new nucleotides - useful as primers in RT-PCR.

Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.4%; Score 10.2; DB 1; Length 16;  
Best Local Similarity 80.0%; Pred. No. 8.4;  
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

16 TGAAGTAAAGAAA 30

16 TGAAGTAAAGAAA 2

## RESULT 9

AA51823

ID AA51823 standard; DNA; 21 BP.

AA51823;

```

FT modified_base 14
PT /*tag= b
TT /mod_base= m5c
XX
XX WO9118997-A.
XX
XX 12-DEC-1991.
XX
XX 25-MAY-1990; 90US-00529346.
XX
XX 25-MAY-1990; 90US-00529346.
XX
XX 14-JAN-1991; 91US-00640654.
XX
XX (GILE-) GILEAD SCIE INC.
XX
XX Matreucci MD, Krawczyk S;
XX
XX WPI; 1992-007480/01.
XX
XX New sequence-specific non-photo-activated crosslinking agents - bind to
XX the major groove of duplex DNA and are esp. useful for treating latent
XX infections e.g. HIV.
XX
XX Example 2; Page 21; 42pp; English.
XX
XX The 3' end of this oligonucleotide carries 1,3-propanediol. The oligo is
XX one of four oligonucleotides which were designed to specifically bind and
XX cross-link to the duplex target sequence AAQ20004. Oligo #4 with its
XX internal cross-linking group was less effective than the other
XX oligonucleotides with terminal cross-linking groups. See also AAQ20005-7
XX
XX Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 3.7;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 462 TTTTTCCTTTTCAT 477
XX 1 TTTTTCCTTTTCCTT 16
XX
XX RESULT 5
XX AA518362
XX ID AA518362 standard; DNA; 16 BP.
XX
XX AA518362;
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 3.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JPI1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
XX PCR.
XX
XX Disclosure; Page 10; 19pp; Japanese.
XX

```

```

CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 14.4; DB 1; Length 16;
XX Best Local Similarity 93.8%; Pred. No. 3.7;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 461 TTTTTCCTTTTCAT 476
XX 1 TTTTTCCTTTTCCTT 16
XX
XX RESULT 6
XX AA51822/C
XX ID AA51822 standard; DNA; 21 BP.
XX
XX AA51822;
XX
XX 31-OCT-2000 (first entry)
XX
XX Sense primer for untreated CASP8 wild type DNA.
XX
XX CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;
XX tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
XX death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2000039347-A1.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031280.
XX
XX 31-DEC-1998; 98US-0114308P.
XX
XX (SUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Kidd VU, Lahti JM, Teitz T;
XX
XX WPI; 2000-452423/39.
XX
XX Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or
XX prognosing cancer, comprises detecting a modification of genomic DNA
XX comprising the CASP8 gene that results in inactivation of the gene.
XX
XX Example 3; Page 61; 107pp; English.
XX
XX Investigation of silencing of caspase-8 (CASP8) gene by methylation was
XX analyzed using methylation-sensitive PCR analysis. Amplification of the
XX 5' untranslated region (5'UTR) of the CASP8 gene was performed in reaction
XX mixtures containing bisulfite treated DNA. Primers AA51818-23 were
XX designed to produce a 320 bp fragment in the upstream region of Casp8
XX gene extending from nucleotides +221 to +541. Wild type primers were used
XX to amplify the corresponding region of untreated genomic DNA. Controls
XX without DNA were also performed. CASP8, a cysteine protease, is part of
XX the death inducing signaling complex (DISC) associated with the Fas
XX receptor. CASP8 is inactivated in cancers, and plays a role of a tumour
XX suppressor gene. The CASP8 promoter region sequences, in particular
XX Region 1 and Region 2, are crucial to the design and execution of the
XX genomic methylation PCR analysis of CASP8 gene inactivation. Methylation

```

PD 06-JUL-2000.  
 XX 30-DEC-1999; 99MO-US031280.  
 XX 31-DEC-1998; 98US-0114308P.  
 PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
 XX Kidd VJ, Lahti JM, Teitz T;  
 XX WPI; 2000-452423/39.  
 DR  
 XX  
 PT Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or  
 PT prognosing cancer, comprises detecting a modification of genomic DNA  
 PT comprising the CASP8 gene that results in inactivation of the gene.  
 XX  
 XX Example 3; Page 61; 107pp; English.  
 PS  
 XX Investigation of silencing of caspase-8 (CASP8) gene by methylation was  
 CC analyzed using methylation-sensitive PCR analysis. Amplification of the  
 CC 5' untranslated region (UTR) of the Casp8 gene was performed in reaction  
 CC mixtures containing bisulfite treated DNA. Primers AA451818-23 were  
 CC designed to produce a 320 bp fragment in the upstream region of Casp8  
 CC gene extending from nucleotides +221 to +541. Wild type primers were used  
 CC to amplify the corresponding region of untreated genomic DNA. Controls  
 CC without DNA were also performed. CASP8, a cysteine protease, is part of  
 CC the death inducing signaling complex (DISC) associated with the Fas  
 CC receptor. CASP8 is inactivated in cancers, and plays a role of a tumour  
 CC suppressor gene. The CASP8 promoter region sequences, in particular  
 CC Region 1 and Region 2, are crucial to the design and execution of the  
 CC genomic methylation PCR analysis of CASP8 gene inactivation. Methylation  
 CC PCR can be used to examine even minute amounts of patient material to  
 CC demonstrate whether the CASP8 gene expresses an mRNA and protein product.  
 CC The CASP8 gene has been localized to human chromosome 2q33-34. The  
 CC methods are used to diagnose or prognose cancer. Cancer is treated by  
 CC administering a vector that expresses a gene encoding functional CASP8 in  
 CC cells. The cancer that is diagnosed or treated is a tumour in which a myc  
 CC gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,  
 CC juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-  
 CC cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma  
 CC can be diagnosed with the new method. A kit for screening for a compound  
 CC that induces death-receptor-mediated apoptosis in cells containing an  
 CC inactivated CASP8 gene is also provided  
 CC  
 XX  
 SQ Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;  
 Query Match 2.8%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 0.52;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 388 CGCCTCGAATGCAGATACACG 408  
 Db 21 CGCCTCGAATGCAGATACACG 1  
 RESULT 3  
 ADE43355  
 ID ADE43355 standard; DNA; 20 BP.  
 XX  
 AC ADE43355;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human uPA primer, SEQ ID 524.  
 XX  
 KW Neurodegenerative disease; uPA; SNG; IDE; KNSL1; LIPA; TNFRSF6;  
 KW Alzheimer's disease; neuroprotective; nootropic; gene therapy;  
 KW Chromosome 10; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003054143-A2.  
 XX

PD 03-JUL-2003.  
 XX 25-OCT-2002; 2002MO-US034679.  
 XX 25-OCT-2001; 2001US-0339525P.  
 PR 08-NOV-2001; 2001US-0336929P.  
 PR 08-NOV-2001; 2001US-0338010P.  
 PR 09-NOV-2001; 2001US-0338363P.  
 PR 04-DEC-2001; 2001US-0337052P.  
 PR 28-MAR-2002; 2002US-0368919P.  
 XX  
 XX (NEUR-) NEUROGENETICS INC.  
 PA (GENO) GEN HOSPITAL CORP.  
 XX  
 PI Becker KD, Velicelbi G, Elliott KJ, Wang X, Tanzi RE, Bertram L;  
 PI Saunders AJ, Mullin KM, Sampson AJ, Blacker DL;  
 XX  
 DR WPI; 2003-559131/52.  
 XX  
 XX Determining a predisposition for or the occurrence of neurodegenerative  
 PT disease, e.g. Alzheimer's disease by detecting in a target nucleic acid  
 PT the presence or absence of an allelic variant of one or more polymorphic  
 PT regions.  
 XX  
 XX Example 4; Page 313; 848pp; English.  
 PS  
 XX The present invention relates to a method (M1) for determining a  
 CC predisposition for or the occurrence of neurodegenerative disease in a  
 CC subject. The method comprises detecting in a target nucleic acid obtained  
 CC from the subject the presence or absence of an allelic variant of one or  
 CC more polymorphic regions of one or more genes selected from uPA  
 CC (uridine kinase plasmidogen activator), SNG (gamma-synuclein), IDE (insulin-  
 CC degrading enzyme), KNSL (Kinesin-like protein 1), LIPA (lysosomal acid  
 CC lipase), and TNFRSF6 (Tumour Necrosis Factor Receptor-SF6), where the  
 CC presence of at least one of the allelic variant of one or more  
 CC polymorphic regions is indicative of a predisposition for or the  
 CC occurrence of neurodegenerative disease. The genes are all located on  
 CC chromosome 10. M1 is useful for determining a predisposition for or the  
 CC occurrence of, and for treating neurodegenerative disease, particularly  
 CC Alzheimer's disease. The present sequence is a PCR primer, which was used  
 CC in the method of the invention.  
 XX  
 SQ Sequence 20 BP; 1 A; 12 C; 2 G; 5 T; 0 U; 0 Other;  
 Query Match 2.4%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 613 TCCCTCCCTGCCCTCG 630  
 Db 3 TCCCTCCCTGCCCTCG 20  
 RESULT 4  
 AAQ20008  
 ID AAQ20008 standard; DNA; 16 BP.  
 XX  
 AC AAQ20008;  
 XX  
 DT 01-APR-1992 (first entry)  
 XX  
 DE Oligonucleotide #4 able to covalently cross-link to target DNA.  
 XX  
 KW deoxyribonucleic acid; major groove; ethanaminio group;  
 KW aziridinylcytosine; cross-linking group; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 8 /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "N4N4-ethanocytosine"

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:10:07 ; Search time 0.001 Seconds  
(without alignments)  
141.564 Million cell updates/sec

Title: us094770822

Perfect score: 753  
Sequence: 1 aatcagaccgcgtatcga...tacatcgcttttaacct 753

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 5 segs, 94 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : 2rng.db\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	2.8	21	AAA51822	Sense primer for u
2	21	2.8	21	AAA51823	Antisense primer f
3	18	2.4	20	ADE43355	Human uPA primer,
4	14.4	1.9	16	AAQ20008	Oligonucleotide #4
5	14.4	1.9	16	AAx18362	RT-PCR primer of t
6	11.6	1.5	21	AAA51822	Sense primer for u
7	10.4	1.4	16	AAQ20008	Oligonucleotide #4
8	10.2	1.4	16	AAx18362	RT-PCR primer of t
9	9.2	1.2	21	AAA51823	Antisense primer f
10	8.6	1.1	20	ADE43355	Human uPA primer,

## ALIGNMENTS

RESULT 1  
ID AAA51822 standard; DNA, 21 BP.

AC AAA51822;  
XX  
XX 31-OCT-2000 (first entry)

XX Sense primer for untreated CASP8 wild type DNA.

DE CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;  
XX tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;  
KW death receptor; apoptosis; cytostatic; gene therapy; primer; ss.

XX Homo sapiens.  
XX  
XX  
XX WO200039347-A1.  
XX

PD 06-JUL-2000.

XX 30-DEC-1999; 99WC-US031280.

XX 31-DEC-1998; 98US-0114308P.

XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Kidd VJ, Lahti JM, Teitz T;

XX WPI; 2000-452423/39.

XX Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or  
PT prognosing cancer, comprises detecting a modification of genomic DNA  
PT comprising the CASP8 gene that results in inactivation of the gene.

XX Example 3; Page 61, 107pp; English.

XX Investigation of silencing of caspase-8 (CASP8) gene by methylation was  
CC analyzed using methylation-sensitive PCR analysis. Amplification of the  
CC 5' untranslated region (UTR) of the Casp8 gene was performed in reaction  
CC mixtures containing bisulfite treated DNA. Primers AAA51818-23 were  
CC designed to produce a 320 bp fragment in the upstream region of Casp8  
CC gene extending from nucleotides 1221 to +541. Wild type primers were used  
CC to amplify the corresponding region of untreated genomic DNA. Controls  
CC without DNA were also performed. CASP8, a cysteine protease, is part of  
CC the death inducing signaling complex (DISC) associated with the Fas  
CC receptor. CASP8 is inactivated in cancers, and plays a role of a tumour  
CC suppressor gene. The CASP8 promoter region sequences, in particular  
CC Region 1 and Region 2, are crucial to the design and execution of the  
CC genomic methylation PCR analysis of CASP8 gene inactivation. Methylation  
CC PCR can be used to examine even minute amounts of patient material to  
CC demonstrate whether the CASP8 gene expresses an mRNA and protein product.  
CC The CASP8 gene has been localized to human chromosome 2q33-34. The  
CC methods are used to diagnose or prognose cancer. Cancer is treated by  
CC administering a vector that expresses a gene encoding functional CASP8 in  
CC cells. The cancer that is diagnosed or treated is a tumour in which a myc  
CC gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma,  
CC juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-  
CC cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma  
CC can be diagnosed with the new method. A kit for screening for a compound  
CC that induces death-receptor-mediated apoptosis in cells containing an  
CC inactivated CASP8 gene is also provided

CC Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

CC Query Match 2.8%; Score 21; DB 1; Length 21;  
CC Best Local Similarity 100.0%; Pred. No. 0.52;  
CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 TAGGGGACTCGGAGACTGCCA 110  
DB 1 TAGGGGACTCGGAGACTGCCA 21

RESULT 2  
ID AAA51823/c  
XX AAA51823 standard; DNA, 21 BP.

AC AAA51823;  
XX  
XX 31-OCT-2000 (first entry)

XX Antisense primer for untreated CASP8 wild type DNA.

DE CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease;  
XX tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;  
KW death receptor; apoptosis; cytostatic; gene therapy; primer; ss.

XX Homo sapiens.  
XX  
XX  
XX WO200039347-A1.  
XX

```

RESULT 27
AR051238/c
LOCUS AR051238 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5830658.
ACCESSION AR051238
VERSION AR051238.1 GI:5974602
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 6 03-NOV-1998;
FEATURES
Source
/mol_type="unassigned DNA"

Query Match 1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAACAAGT 653
DB 11 AAAAAAAAAAGT 1

RESULT 28
I16032/c
LOCUS I16032 16 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION I16032
VERSION I16032.1 GI:1250940
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES
Source
/mol_type="unassigned DNA"

Query Match 1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAACAAGT 653
DB 11 AAAAAAAAAAGT 1

RESULT 29
I28367/c
LOCUS I28367 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION I28367
VERSION I28367.1 GI:1819143
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures

```

```

JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES
Source
/mol_type="unassigned DNA"

Query Match 1.2%; Score 9.4; DB 1; Length 16;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAACAAGT 653
DB 11 AAAAAAAAAAGT 1

RESULT 30
AR231294/c
LOCUS AR231294 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 31 from patent US 6451968.
ACCESSION AR231294
VERSION AR231294.1 GI:2727225
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Esholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coul,J.M., Kieley,J. and Griffith,M.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6451968-A 31 17-SEP-2002;
FEATURES
Source
/mol_type="genomic DNA"

Query Match 1.2%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 AAGTAAAGAA 29
DB 14 AAGGAAAAAAAA 3

Search completed: March 31, 2004, 14:08:57
Job time : 1 secs

```

QY 640 CCAAAAACAG 652  
 Db 4 CCAAAAACAG 16

RESULT 22  
 LOCUS 149619 16 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 34 from patent US 5641625.  
 ACCESSION 149619  
 VERSION 149619.1 GI:2471839  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Becker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Møllegaard,N.E.  
 TITLE Cleaving double-stranded DNA with peptide nucleic acids  
 JOURNAL Patent: US 5641625-A 34 24-JUN-1997;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
 Best Local Similarity 84.6%; Pred. No. 25;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
 Db 4 CCAAAAACAG 16

RESULT 23  
 LOCUS AR200478 16 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 21 from patent US 6357163.  
 ACCESSION AR200478  
 VERSION AR200478.1 GI:20251366  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
 TITLE Use of nucleic acid analogues in diagnostics and analytical procedures  
 JOURNAL Patent: US 6357163-A 21 19-MAR-2002;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
 Best Local Similarity 84.6%; Pred. No. 25;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
 Db 4 CCAAAAACAG 16

RESULT 24  
 LOCUS AR371265 16 bp DNA linear PAT 12-SEP-2003  
 DEFINITION Sequence 1 from patent US 6395474.  
 ACCESSION AR371265  
 VERSION AR371265.1 GI:34608197  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
 TITLE Peptide nucleic acids  
 JOURNAL Patent: US 6395474-A 1 28-MAY-2002;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
 Best Local Similarity 84.6%; Pred. No. 25;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 CCAAAAACAG 652  
 Db 4 CCAAAAACAG 16

RESULT 25  
 LOCUS AR002257/c 16 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 6 from patent US 5741643.  
 ACCESSION AR002257  
 VERSION AR002257.1 GI:3963811  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
 TITLE Oligonucleotide clamps  
 JOURNAL Patent: US 5741643-A 6 21-APR-1998;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.2%; Score 9.4; DB 1; Length 16;  
 Best Local Similarity 90.9%; Pred. No. 27;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAACAGT 653  
 Db 11 AAAAAACAGT 1

RESULT 26  
 LOCUS AR045207/c 16 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 6 from patent US 5617795.  
 ACCESSION AR045207  
 VERSION AR045207.1 GI:5966672  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
 TITLE Oligonucleotide clamps having diagnostic and therapeutic applications  
 JOURNAL Patent: US 5617795-A 6 06-OCT-1998;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.2%; Score 9.4; DB 1; Length 16;  
 Best Local Similarity 90.9%; Pred. No. 27;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 643 AAAAAACAGT 653  
 Db 11 AAAAAACAGT 1

AUTHORS	Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Møllgaard,N.E.
TITLE	Peptide nucleic acids complexes of two peptide nucleic acid strands and one nucleic acid strand
JOURNAL	Patent: US 5986053-A 34 16-NOV-1999;
FEATURES	Location/Qualifiers
source	1..16 /organism="unknown" /mol_type="unassigned DNA"
QY	640 CCCAAAAACAG 652     4 CCAAAAAAAAAAG 16
RESULT 18	
LOCUS	ARI50597 16 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 9 from patent US 6228982.
ACCESSION	ARI50597
VERSION	ARI50597.1 GI:15115188
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 16) Norden,B., Wiltung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R. Double-stranded peptide nucleic acids Patent: US 6228982-A 9 08-MAY-2001; location/Qualifiers 1..16 /organism="unknown" /mol_type="unassigned DNA"
MATCHES	Query Match 1.3%; Score 9.8; DB 1; Length 16; Best Local Similarity 84.6%; Pred. No. 25; Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	640 CCCAAAAACAG 652       4 CCAAAAAAAAAAG 16
Db	
RESULT 19	
LOCUS	E36063 16 bp DNA linear PAT 18-JUN-2001
DEFINITION	Higher-order structure and binding of peptide nucleic acid.
ACCESSION	E36063
VERSION	E36063.1 GI:13022465
KEYWORDS	JP 1999236396-A/8.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	1 (bases 1 to 16) Bushart,O., Eguchiura,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and Moragado,N.A. Higher-order structure and binding of peptide nucleic acid Patent: JP 1999236396-A 8 31-AUG-1999; ISIS PHARMACEUTICALS INC, BUCHARDT DORUTE, EGUCHIURU MICHAEL, IEISEN PATER A, BERG RORUFU HO PATER A, BERG RORUFU HO OS Unidentified PN JP 1999236396-A/8 PD 31-AUG-1999 PF 14-OCT-1998 JP 1998291590 PR 02-JUL-1993 US 088658 PI BUSHART ORE, EGUCHIURU MICHAEL, NIELSEN PATER A, BERG RORUFU HO, PI EKKA DAVID JAY, MORAGADO NILUS A PC C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,
COMMENT	

```

FEATURES
source
    Query Match      1.3%; Score 9.8; DB 1; Length 16;
    Best Local Similarity 84.6%; Pred. No. 25;
    Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

    Oy      640 CCGAAAAACAG 652
           |||||
           4 CCAAAAAAAAAAG 16

    RESULT 20
    LOCUS      142181                      16 bp     DNA          PAT 07-OCT-1997
    DEFINITION Sequence 16 from patent US 5629152.
    ACCESSION   I42181
    VERSION     I42181.1 GI:2467676
    KEYWORDS
    SOURCE      Unknown.
    ORGANISM    Unkown.
    REFERENCES   1 (bases 1 to 16)
                Ravikumar, V.
                Trisubstituted .beta.-lactams and oligo .beta.-lactamides
                Patent: US 5629152-A 16 13-MAY-1997;
                Location/Qualifiers
                    1..16
                        /organism='unknown'
                        /mol_type='unassigned DNA'

    QUERY MATCH
    LOCUS      142187                      16 bp     DNA          linear       PAT 07-OCT-1997
    DEFINITION Sequence 25 from patent US 5629152.
    ACCESSION   I42187
    VERSION     I42187.1 GI:2467682
    KEYWORDS
    SOURCE      Unknown.
    ORGANISM    Unkown.
    REFERENCES   1 (bases 1 to 16)
                Ravikumar, V.
                Trisubstituted .beta.-lactams and oligo .beta.-lactamides
                Patent: US 5629152-A 25 13-MAY-1997;
                Location/Qualifiers
                    1..16
                        /organism='unknown'
                        /mol_type='unassigned DNA'

    FEATURE
    source
        Query Match      1.3%; Score 9.8; DB 1; Length 16;
        Best Local Similarity 84.6%; Pred. No. 25;
        Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

        Oy      640 CCGAAAAACAG 652
             |||||
             4 CCAAAAAAAAAAG 16

        Db      4 CCAAAAAAAAAAG 16

```

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 4.3;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGTGATC 730  
 Db 16 CTTTCTTTTGTGATC 1

RESULT 13  
 AR200478/c 16 bp DNA linear PAT 20-APR-2002  
 LOCUS AR200478  
 DEFINITION Sequence 21 from patent US 6357163.  
 ACCESSION AR200478  
 VERSION AR200478.1 GI:20251366  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
 TITLE Use of nucleic acid analogues in diagnostic and analytical procedures  
 JOURNAL Patent: US 6357163-A 21 19-MAR-2002;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 4.3;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGTGATC 730  
 Db 16 CTTTCTTTTGTGATC 1

RESULT 14  
 AR371265/c 16 bp DNA linear PAT 12-SEP-2003  
 LOCUS AR371265  
 DEFINITION Sequence 1 from patent US 6395474.  
 ACCESSION AR371265  
 VERSION AR371265.1 GI:34608197  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.  
 TITLE Peptide nucleic acids  
 JOURNAL Patent: US 6395474-A 1 28-MAY-2002;  
 FEATURES Location/Qualifiers  
 1..16  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
 Best Local Similarity 93.8%; Pred. No. 4.3;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGTGATC 730  
 Db 16 CTTTCTTTTGTGATC 1

RESULT 15  
 AR331294 15 bp DNA linear PAT 20-DEC-2002  
 LOCUS AR331294  
 DEFINITION Sequence 31 from patent US 6451968.  
 ACCESSION AR331294  
 VERSION AR331294.1 GI:27272225

KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,  
 Coull,J.M., Kiely,J. and Griffith,M.  
 TITLE Peptide nucleic acids  
 JOURNAL Patent: US 6451968-A 31 17-SEP-2002;  
 FEATURES Location/Qualifiers  
 1..15  
 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 1.9%; Score 14; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 CTTTCTTTTCTTTT 473  
 Db 2 CTTTCTTTTCTTTT 15

RESULT 16  
 A36563 16 bp DNA linear PAT 05-MAR-1997  
 LOCUS A36563  
 DEFINITION Sequence 3 from Patent WO9325706.  
 ACCESSION A36563  
 VERSION A36563.1 GI:2293876  
 KEYWORDS  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 16)  
 AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Stanley,C.J.  
 TITLE USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF NUCLEIC ACID AMPLIFICATION  
 JOURNAL Patent: WO 9325706-A 3 23-DEC-1993;  
 BUCHARDT OLE (DX)  
 COMMENT Other publication CZ 9402951 950913  
 Other publication AU 4323593 940104  
 Other publication CA 2136831 931223  
 Other publication SK 149394 960110  
 Other publication HU 71931 960228  
 Other publication FI 945725 941205  
 Other publication NO 944655 950203  
 Other publication JP 8501681T 960227.

FEATURES Location/Qualifiers  
 1..16  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

Query Match 1.3%; Score 9.8; DB 1; Length 16;  
 Best Local Similarity 84.6%; Pred. No. 25;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 640 CCCAAAACACAG 652  
 Db 4 CCCAAAACACAG 16

RESULT 17  
 AR087164 16 bp DNA linear PAT 07-SEP-2000  
 LOCUS AR087164  
 DEFINITION Sequence 34 from patent US 5986053.  
 ACCESSION AR087164  
 VERSION AR087164.1 GI:10013327  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)

## source

1. .16  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGGATC 730  
Db 16 CTTTCTTTTGGATC 1

## RESULT 8

LOCUS 116032 16 bp DNA linear PAT 03-APR-1996  
DEFINITION Sequence 6 from patent US 5473060.  
ACCESSION 116032  
VERSION 116032.1 GI:1250940  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps having diagnostic applications  
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;  
FEATURES Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 459 ACTTTTCTTTT 474  
Db 1 ACTTTTCTTTT 16

RESULT 9  
LOCUS 128367 16 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 6 from patent US 5571677.  
ACCESSION 128367  
VERSION 128367.1 GI:1819143  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Gryaznov,S.M.  
TITLE Convergent synthesis of branched and multiply connected  
macromolecular structures  
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;  
FEATURES Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 459 ACTTTTCTTTT 474  
Db 1 ACTTTTCTTTT 16

RESULT 10  
142181/c

LOCUS 142181 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 16 from patent US 5629152.  
ACCESSION 142181  
VERSION 142181.1 GI:2467676  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Ravikumar,V.  
TITLE Trisubstituted .beta.-lactams and oligo .beta.-lactamamides  
JOURNAL Patent: US 5629152-A 16 13-MAY-1997;  
FEATURES Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGGATC 730  
Db 16 CTTTCTTTTGGATC 1

RESULT 11  
LOCUS 142187 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 25 from patent US 5629152.  
ACCESSION 142187  
VERSION 142187.1 GI:2467682  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Ravikumar,V.  
TITLE Trisubstituted .beta.-lactams and oligo .beta.-lactamamides  
JOURNAL Patent: US 5629152-A 25 13-MAY-1997;  
FEATURES Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CTTTCTTTTGGATC 730  
Db 16 CTTTCTTTTGGATC 1

RESULT 12  
LOCUS 149619 16 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 34 from patent US 5641625.  
ACCESSION 149619  
VERSION 149619.1 GI:2471839  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Ecker,D.U., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Møllegaard,N.E.  
TITLE Cleaving double-stranded DNA with peptide nucleic acids  
JOURNAL Patent: US 5641625-A 34 24-JUN-1997;  
FEATURES Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

ACCESSION AR045207  
VERSION AR045207.1 GI:5966672  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassefied.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Gryaznov,S.M. and Lloyd,D.H.  
TITLE Oligonucleotide clamps having diagnostic and therapeutic applications  
JOURNAL Patent: US 5817795-A 6 06-OCT-1998;  
FEATURES Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTCTCTTTT 474  
DB 1 ACTTTTCTCTTTT 16

RESULT 4  
LOCUS AR051238 16 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 6 from patent US 5830658.  
ACCESSION AR051238  
VERSION AR051238.1 GI:5974602  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassefied.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Gryaznov,S.M.  
TITLE Convergent synthesis of branched and multiply connected macromolecular structures  
JOURNAL Patent: US 5830658-A 6 03-NOV-1998;  
FEATURES Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 459 ACTTTTCTCTTTT 474  
DB 1 ACTTTTCTCTTTT 16

RESULT 5  
LOCUS AR087164 16 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 34 from patent US 5986053.  
ACCESSION AR087164  
VERSION AR087164.1 GI:10013927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassefied.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.  
TITLE Peptide nucleic acids complexes of two peptide nucleic acid strands and one nucleic acid strand  
JOURNAL Patent: US 5986053-A 34 16-NOV-1999;  
FEATURES Location/Qualifiers  
1..16  
/organism="unknown"

/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGGATC 730  
DB 16 CTTTTTTTGGATC 1

RESULT 6  
LOCUS AR150597 16 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 9 from patent US 6228982.  
ACCESSION AR150597  
VERSION AR150597.1 GI:15115188  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassefied.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Norden,B., Wiltung,P., Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.  
TITLE Double-stranded peptide nucleic acids  
JOURNAL Patent: US 6228982-A 9 08-MAY-2001;  
FEATURES Location/Qualifiers  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CTTTTTTTGGATC 730  
DB 16 CTTTTTTTGGATC 1

RESULT 7  
LOCUS E36063 16 bp DNA linear PAT 18-JUN-2001  
DEFINITION Higher-order structure and binding of peptide nucleic acid.  
ACCESSION E36063  
VERSION E36063.1 GI:13022465  
KEYWORDS JP 1999236396-A/8.  
SOURCE unidentified  
ORGANISM unclassefied.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Bushato,O., Egholm,M., Nielsen,P.A., Berg,R.H., Ekka,D.J. and Morugado,N.A.  
TITLE Higher-order structure and binding of peptide nucleic acid  
JOURNAL Patent: JP 1999236396-A 8 31-AUG-1999;  
JOURNAL ISIS PHARMACEUTICALS INC,BUCHARDT DORUTE,EGHORUMU MICHAEL, IELSEN PATER A, BERG RORUFU HO  
OS Unidentified  
FN Unidentified  
PD JP 1999236396-A/8  
PF 14-OCT-1998 JP 1998291590  
PR 02-JUL-1993 US 088658  
PI BUSHATO ORE,EGHORUMU MICHAEL,NIELSEN PATER A,BERG RORUFU HO,  
PC EKKAD DAVID JAY MORUGADO NILUS A  
PC C07H21/04,A61K31/00,A61K31/00,A61K31/00,A61K31/70,A61K48/00,  
PC C07H21/02  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..16  
/organism="Unidentified".  
FEATURES Location/Qualifiers

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:08:56 ; Search time 0.001 Seconds  
(without alignments)  
359.934 Million cell updates/sec

Title: us094770822

Perfect score: 753  
Sequence: 1 aattagccgcgtattgaaa.....tacctgttttttaacct 753

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 15 segs, 239 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : 2rge.db:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.4	1.9	16	A36563	ACCESSION:A36563
C 2	14.4	1.9	16	AR002257	ACCESSION:AR002257
C 3	14.4	1.9	16	AR045207	ACCESSION:AR045207
C 4	14.4	1.9	16	AR051238	ACCESSION:AR051238
C 5	14.4	1.9	16	AR087164	ACCESSION:AR087164
C 6	14.4	1.9	16	AR150597	ACCESSION:AR150597
C 7	14.4	1.9	16	E36063	ACCESSION:E36063
C 8	14.4	1.9	16	E116032	ACCESSION:E116032
C 9	14.4	1.9	16	I128367	ACCESSION:I128367
C 10	14.4	1.9	16	I42181	ACCESSION:I42181
C 11	14.4	1.9	16	I42187	ACCESSION:I42187
C 12	14.4	1.9	16	I49619	ACCESSION:I49619
C 13	14.4	1.9	16	AR200478	ACCESSION:AR200478
C 14	14.4	1.9	16	AR371265	ACCESSION:AR371265
C 15	14.4	1.9	16	AR231294	ACCESSION:AR231294
C 16	9.8	1.3	16	A36563	ACCESSION:A36563
C 17	9.8	1.3	16	AR087164	ACCESSION:AR087164
C 18	9.8	1.3	16	AR150597	ACCESSION:AR150597
C 19	9.8	1.3	16	E36063	ACCESSION:E36063
C 20	9.8	1.3	16	I42181	ACCESSION:I42181
C 21	9.8	1.3	16	I42187	ACCESSION:I42187
C 22	9.8	1.3	16	I49619	ACCESSION:I49619
C 23	9.8	1.3	16	AR200478	ACCESSION:AR200478
C 24	9.8	1.3	16	AR371265	ACCESSION:AR371265
C 25	9.8	1.3	16	AR002257	ACCESSION:AR002257
C 26	9.4	1.2	16	AR045207	ACCESSION:AR045207
C 27	9.4	1.2	16	AR051238	ACCESSION:AR051238
C 28	9.4	1.2	16	AR051238	ACCESSION:AR051238
C 29	9.4	1.2	16	I16032	ACCESSION:I16032
C 30	8.8	1.2	16	I28367	ACCESSION:I28367
C 30	8.8	1.2	16	AR231294	ACCESSION:AR231294

## ALIGNMENTS

RESULT 1  
LOCUS A36563/c 16 bp DNA linear PAT 05-MAR-1997  
DEFINITION Sequence 3 from Patent WO9325706.  
ACCESSION A36563  
VERSION A36563.1 GI:2293876  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Buchardt, O., Espholm, M., Nielsen, P.E., Berg, R.H. and Stanley, C.J.  
TITLE USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION OF NUCLEIC ACID  
AMPLIFICATION  
JOURNAL Patent: WO 9325706-A 3 23-DEC-1993;  
COMMENT BUCHARDT OLE (DK)  
Other publication CZ 9402951 950913  
Other publication AU 4323593 940104  
Other publication CA 2136831 931223  
Other publication SK 149394 960110  
Other publication HU 71931 960228  
Other publication FI 945725 941205  
Other publication NO 944655 950203  
Other publication JP 8501681T 960227.  
FEATURES  
source  
1..16  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 715 CTTTTTTTTTGATC 730  
Db 16 CTTTTTTTTTGATC 1

RESULT 2  
LOCUS AR002257 16 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 6 from patent US 5741643.  
ACCESSION AR002257  
VERSION AR002257.1 GI:3963811  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Gryaznov, S.M. and Lloyd, D.H.  
TITLE Oligonucleotide clamps  
JOURNAL Patent: US 5741643-A 6 21-APR-1998;  
FEATURES  
source  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.9%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 4.3;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 459 ACTTTTTTTCTTTT 474  
Db 1 ACTTTTTTTT 16

RESULT 3  
LOCUS AR045207 16 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 6 from patent US 5817795.

PT respectively, for targeting sequences on alternate strands of DNA to  
 PT control gene expression.

XX  
 PS Example 2; Fig 4B; 108pp; English.

CC The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the  
 CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents an oligonucleotide used in the  
 CC methods of the present invention

XX  
 SQ Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 8.2; DB 1; Length 15;

Best Local Similarity 76.9%; Pred. No. 0;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 255 AGCGAAGAGGAAA 267

DB 15 AGAGAAAGAGAAA 3

Search completed: March 31, 2004, 14:06:04  
 Job time : 0.001 secs

```

XX MPI, 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX
XX Example 2; Fig 4B; 108bp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences regulated by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or repressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention
XX
XX Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 2.1%; Score 14; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred.No. 0;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 550 TTTTCTCTTCTCT 563
XX |||||
XX 2 TTTTCTCTTCTCT 15
XX
XX RESULT 3
XX AAH20313/C
XX ID AAH20313 standard; DNA; 15 BP.
XX
XX AAH20313;
XX
XX 31-JUL-2001 (first entry)
XX
XX DNA-EDTA-FE(II) probe 7.
XX
XX Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX
XX Synthetic.
XX
XX OS
XX
XX Key Location/Qualifiers
XX modified_base 5
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note="Thymidine has EDTA-FE(II) covalently attached at
XX C-5"
XX
XX US2001002314-A1.
XX
XX 31-MAY-2001.
XX
XX 04-AUG-1998; 98US-00128732.
XX
XX 30-OCT-1987; 87US-00115922.

```

```

PR    16-NOV-1990;      90US--00614205.
PR    12-NOV-1993;     93US--00152250.
XX
PA    (FLEH-) FLEHR HOHBACH TEST ALBERTTON & HERBERT.
XX
PI    Dervan PB, Moser HE;
XX
DR    WPI, 2001-342909/36.
XX
PT    New hybridization probe for specific triplex formation with large double
PT    helices, useful e.g. for site-specific diagnostic cleavage, contains
PT    attached functional residue.
XX
PS    Example 2; Fig 4B; 20PD; English.
XX
CC    This invention relates to hybridisation probes which target a specific
CC    sequence within a large double-helical nucleic acid. The probe is
CC    complementary to the target sequence and contains at least one nucleotide
CC    with an attached molecule that is able to cleave double-helical DNA e.g.
CC    EDTA-Pe(II) (ethylenediaminetetraacetic acid-iron complex). The probes
CC    where the attached molecule is a label or compound that alters gene
CC    expression, are used for specific detection and/or cleavage of double-
CC    helical DNA, e.g. for diagnosis, for treatment of disease (particularly
CC    caused by viruses, genetic defects or oncogenes), for chromosomeal
CC    analysis, and for the isolation and mapping of genes. The present
CC    sequence represents a probe of the invention which is used in an example
CC    illustrating how it binds to and cleaves a double stranded fragment of
CC    plasmid pDMAG10 given in AH20315
XX
SQ    Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
XX
Query Match          1.2%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX
QY        255 AGGCAAGCGAAA 267
           ||| ||||| |||
Db         15 AGAGAAAGAGAAA 3
XX
RESULT 4
ABK98147/C
ID ABK98147 standard; DNA; 15 BP.
XX
AC ABK98147;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #30.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US--00168920.
XX
PR 17-SEP-1993; 92US--00946976.
XX
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Seal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation.
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:06:04 ; Search time 0.001 Seconds  
(without alignments)  
40.200 Million cell updates/sec

Title: us094770821

Perfect score: 670  
Sequence: 1 aagcgtccagacacgalt.....599gttaataaagcgtt 670

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 30 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 20 summaries

Database : 1rng.db:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	2.1	15	AAH20313	DNA-EDTA-FE(II) pr
2	14	2.1	15	ABK98147	Triple helix form
3	8.2	1.2	15	AAH20313	DNA-EDTA-FE(II) pr
4	8.2	1.2	15	ABK98147	Triple helix form

## ALIGNMENTS

RESULT 1  
AAH20313  
ID AAH20313 standard; DNA; 15 BP.  
XX  
AC AAH20313;  
XX  
DT 3i-JUL-2001 (first entry)  
XX  
DE DNA-EDTA-FE(II) probe 7.  
XX  
KM Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.  
XX  
OS Synthetic.  
XX  
FH Key  
FT modified\_base 5 Location/Qualifiers  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Thymidine has EDTA-FE(II) covalently attached at C-5"  
XX  
XX US2001002314-A1.  
XX  
XX 31-MAY-2001.  
PD

XX 04-AUG-1998; 98US-00128732.  
XX  
XX 30-OCT-1987; 87US-00115922.  
XX  
XX 16-NOV-1990; 90US-00614205.  
XX  
XX 12-NOV-1993; 93US-00152250.  
XX  
XX (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.  
XX  
XX Dervan PB, Moser HE;  
XX  
XX WPI; 2001-342909/36.  
XX  
XX  
XX New hybridization probe for specific triple helix formation with large double  
XX helices, useful e.g. for site-specific diagnostic cleavage, contains  
XX attached functional residue.  
XX  
XX Example 2; Fig 4B; 20p; English.  
XX  
XX This invention relates to hybridisation probes which target a specific  
XX sequence within a large double-helical nucleic acid. The probe is  
XX complementary to the target sequence and contains at least one nucleotide  
XX with an attached molecule that is able to cleave double-helical DNA e.g.  
XX EDTA-FE(II) (ethylenediaminetetraacetic acid-iron complex). The probe  
XX where the attached molecule is a label or compound that alters gene  
XX expression, are used for specific detection and/or cleavage of double-  
XX helical DNA, e.g. for diagnosis, for treatment of disease (particularly  
XX caused by viruses, genetic defects or oncogenes), for chromosomal  
XX analysis, and for the isolation and mapping of genes. The present  
XX sequence represents probe of the invention which is used in an example  
XX illustrating how it binds to and cleaves a double stranded fragment of  
XX plasmid pMDA10 given in AAH20313  
XX  
XX Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;  
XX  
XX Query Match 2.1%; Score 14; DB 1; Length 15;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Oy 550 TTTTCTTTTCTCT 563  
XX  
XX Db 2 TTTTCTTTTCTCT 15  
XX  
XX  
XX RESULT 2  
XX ABK98147  
XX ID ABK98147 standard; DNA; 15 BP.  
XX  
XX AC ABK98147;  
XX  
XX DT 07-OCT-2002 (first entry)  
XX  
XX DE Triple helix forming associated oligonucleotide #30.  
XX  
XX KM Triple-helix formation; purine-rich target sequence; double-helix DNA;  
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;  
XX pathogenic bacteria; virus; replication; virulence; cancer;  
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN US6403302-B1.  
XX  
XX PD 11-JUN-2002.  
XX  
XX PF 16-DEC-1993; 93US-00168920.  
XX  
XX PR 17-SEP-1992; 92US-00946976.  
XX  
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
XX Dervan PB, Beal PA;  
XX  
XX

Initial Score = 7 Optimized Score = 13 Significance = -0.25  
Residue Identity = 52% Matches = 13 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

CTGAAGGGGTTTCCTTTATGTCTCCACCCCAACCTTCCCTCCCTGCTGTGTTTGGCCAAA  
580 590 600 610 620 630 640  
X  
AAACAAGTCTCTAAACGTTTCGATGCGATCGGAGAAATTACCTGCAC  
650 660 670 680 690  
X  
CNA  
X

29. US-09-477-082-2 (1-753)  
US-09-477-082-34 Sequence 34, Application US/09477082

Initial Score = 6 Optimized Score = 12 Significance = -0.26  
Residue Identity = 57% Matches = 12 Mismatches = 9  
Gaps = 0 Conservative Substitutions = 0

TTTGTTCCTTCTGCTCTAGAAACAGGGCTGGGGGTGGGAGCAACTGGATCGCCCTTCTAGGA  
190 200 210 220 230 240 250 X  
X  
CACCTGTGCTGTGCTGGCCCAAGGTCTCTCTGTGTGTTCTCTCTGAG  
260 270 280 290 300  
X  
CGTGTATCTGCATTGAGCG  
X 10 20

30. US-09-477-082-2 (1-753)  
US-09-477-082-18 Sequence 18, Application US/09477082

Initial Score = 6 Optimized Score = 11 Significance = -0.26  
Residue Identity = 52% Matches = 11 Mismatches = 10  
Gaps = 0 Conservative Substitutions = 0

CTCTCTGAGCCGATGCTTGTGACTTTTCACTTTCACTGTGAGCAGTCTCTGCTACCTTTT  
300 310 320 330 340 350 360 X  
X  
TTCCTCTCTCTTACACCTG  
X 10 20

370 380 390 400 410  
TGTCTTCAAGCTTCCCTGCGCTCGATGCAGATACAGGACTCCCT

31. US-09-477-082-2 (1-753)  
US-09-477-082-22 Sequence 22, Application US/09477082

Initial Score = 6 Optimized Score = 10 Significance = -0.26  
Residue Identity = 43% Matches = 10 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0

530 540 550 560 570 580 590  
X  
GATTCGGAATGCCCTGAGGTGACAGCCCTTCCCTCTTCCGCTCTGAGAGGGTTTCTTTATGTC  
600 610 620 630 640  
TTCCACCCCACTTCCCTCCCTCCGCTCTGCTTTTGTGCCCCAAA  
X  
TCCCGGTTTCCCGAGGGGA  
X 10 20

Initial Score = 5 Optimized Score = 11 Significance = -0.27  
Residue Identity = 50% Matches = 11 Mismatches = 11  
Gaps = 0 Conservative Substitutions = 0

AATTAGCGCGTATTGAAGTAAGAACTTCTCTGGAGCCTTCCACCCCTTCCCTGCTAGCA  
10 20 30 40 50 60 70  
X  
CGTATATCTACATTGAAACGA  
X 10 20 X  
CGTGGAGT  
80

32. US-09-477-082-2 (1-753)  
US-09-477-082-30 Sequence 30, Application US/09477082

G  
X

## 20. US-09-477-082-2 (1-753)

US-09-477-082-25 Sequence 25, Application US/09477082

Initial Score = 10 Optimized Score = 10 Significance = -0.23  
Residue Identity = 50% Matches = 10 Mismatches = 10  
Gaps = 0 Conservative Substitutions = 0

620 630 640 650 660 670 680 X  
CCCTGCCCTCTGTTTGTGTCACAAAAACAAGTTCTTAAACGTTTTCAGTGTGCGGAAATTA  
GATGCGGTGGCGGCGCTC  
X 10 20

700 710 720 730  
ACCTGCACCCGTTTGCAAAATGAATCTTTTGTGATCCGTACAC

## 21. US-09-477-082-2 (1-753)

US-09-477-082-21 Sequence 21, Application US/09477082

Initial Score = 10 Optimized Score = 14 Significance = -0.23  
Residue Identity = 60% Matches = 14 Mismatches = 9  
Gaps = 0 Conservative Substitutions = 0

450 460 470 480 490 500 510  
AAGAAGCTTATCAATCCACTTTTCTTTCTTTGATTTGGCCCGGCGGAGGTTAGTACTTATTC  
TCAATGTAGTTAATTACTA  
X 10 20

X 520 530 540 550 560  
TGTCAATCTGTGAATCAGAAATGCCCTGAGGACACACCCCTTCCCT

T  
X

## 22. US-09-477-082-2 (1-753)

US-09-477-082-28 Sequence 28, Application US/09477082

Initial Score = 9 Optimized Score = 13 Significance = -0.24  
Residue Identity = 59% Matches = 13 Mismatches = 9  
Gaps = 0 Conservative Substitutions = 0

380 390 400 410 420 430 440 X  
CCTCCAAAGCTTCCCTGCCGCTGAGATGACAGATACGAGATCCCTTCTGTGACCCGTTGAGAGTCCAG  
GTGAATAGTTGCAAGGCGAT  
X 10 20 X

450 460 470 480 490  
AAGACTTATCAATCCACTTTTCTTTCTTTTCAATTTGGCCCTGCGGCGC

## 23. US-09-477-082-2 (1-753)

US-09-477-082-15 Sequence 15, Application US/09477082

Initial Score = 9 Optimized Score = 12 Significance = -0.24  
Residue Identity = 54% Matches = 12 Mismatches = 10  
Gaps = 0 Conservative Substitutions = 0

170 180 190 200 210 X 220 230 X  
TTCAACAGGAACCAATATTTTCTTTCTTTGACTTGTAGAAACAGGCTGTGGGAGGAGAAACAA  
GCTTACAGGTTGGGAGAACTC  
X 10 20 X

240 250 260 270 280  
CTTGATCTGCTTCTGAGAGACCTGTGTGCTGCTGGCCAGGTCT

## 24. US-09-477-082-2 (1-753)

US-09-477-082-16 Sequence 16, Application US/09477082

Initial Score = 8 Optimized Score = 9 Significance = -0.24  
Residue Identity = 45% Matches = 9 Mismatches = 11  
Gaps = 0 Conservative Substitutions = 0

120 130 140 150 160 X 170 X  
GCTCCAGAAAGAGTGAAGCGGATGATGCTGTTGCCAAGGTGAGCTTCAACAGAAACCAATATT  
CCCAACCAAAAGGTCATG  
X 10 20

190 200 210 220 230  
TTTGTCTTGACTGCTGTAGAAACAGAGGCTGTGGGAGGAGGAGC

## 25. US-09-477-082-2 (1-753)

US-09-477-082-23 Sequence 23, Application US/09477082

Initial Score = 8 Optimized Score = 9 Significance = -0.24  
Residue Identity = 42% Matches = 9 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

290 300 310 320 330 340 X  
TCTCCTGTGTGTTCTCTCTGAGCCGATGCTTGTGACTTGTGACTTGTGACTCTGAGAGTCCAGTT  
TCAAGGTACGAGAAAC  
X 10 20

360 370 380 390 400  
CCTCTGCTACCTTTTGTCTCCCAAGCTTCCCTGCGCGCTGAGATGAG

## 26. US-09-477-082-2 (1-753)

US-09-477-082-20 Sequence 20, Application US/09477082

Initial Score = 8 Optimized Score = 11 Significance = -0.24  
Residue Identity = 52% Matches = 11 Mismatches = 10  
Gaps = 0 Conservative Substitutions = 0

190 200 210 220 230 240 250 X  
TTCTTACTTCTCTAAGAACAGGCTGTGGGAGTGAACACTTGAATCTGCTTGTGAGCACTT  
TTTGCTTATCTGAGAGAGA  
X 10 20

270 280 290 300  
CTGTGCTGCTGCGCCAGAGTCTCTGTGTGCTTCTCTGAGCCGAT

## 27. US-09-477-082-2 (1-753)

US-09-477-082-17 Sequence 17, Application US/09477082

Initial Score = 8 Optimized Score = 14 Significance = -0.24  
Residue Identity = 66% Matches = 14 Mismatches = 7  
Gaps = 0 Conservative Substitutions = 0

50 70 80 90 100 X 110 X 120 X  
CCCCCTTCCCTGCTGAGACAGTGAAGTTAGGAGGACTGAGGAGCTCGAGTGTGCGAGAAAGG  
GATGACATGCTGCTGGAGAC  
X 10 20

130 140 150 160 170  
GTGAGCGGAGTGAAGCTGTGTGCCAAGGTGCTTTCACAGAGAAAC

## 28. US-09-477-082-2 (1-753)

US-09-477-082-32 Sequence 32, Application US/09477082







[illegible]

4. US-09-477-082-2 (1-753)  
US-09-477-082-3 Sequence 3, Application US/09477082

Initial Score	=	35	Optimized Score	=	236	Significance	=
Residue Identity	=	36%	Matches	=	305	Mismatches	=
Gaps	=	84	Conservative Substitutions	=			

10 20 30 40 50 60 70  
 CCACGCGCCGACGCCCATTTGCGTGTGTTGTAATGTCATCTTCCCTTAACAGTAAGAGGAGCACTGTCGTGTG  
 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150  
 GCGCTTCCCAACCCCTTCCCTCCCTGCTGAGACCTGAGATTAGGCAAGTTAGGGACTGGAGACTGCATGTC  
 TCTTTTCTCTCTCTCTGCGCTGACAGCAACATGACCAAGTACCTAGTGTGTCAGTGCCTTTATGTAACA  
 120 130 140 150 160  
 CAGGAAAGAGGTGAGCGGAGTGAAGCTCTGTGGCAAGT GGCCTCT  
 CAGGAAAGTGAAGTCTTTCTTCCTATATGAAACATACATTTATTTTGACTAGATTATATCTCGTGCCT  
 150 160 170 180 190 200 210

TTCAACAG	170	180	190	200	210	220
-----GAAACCA	180	190	200	210	220	
CAATATTTTGT	190	200	210	220		
CTTCTTCACTG	200	210	220			
CTTGTGAAAC	210	220				
AGGGGTGGGG	220					
GTGGG						
TTAAAGATG	230	240	250	260	270	280
ACTTCAGCA	240	250	260	270	280	
AAATCTTTTGT	250	260	270	280		
ATTGGGAACA	260	270	280			
CACTGACAC	270	280				
AGAGATCTGG	280					
CCCTCC						
GAAG	240	250	260	270	280	
CAACTTGAT	250	260	270	280		
CTGCCCTCTG	260	270	280			
AGACACCT	270	280				
CTGTGCTGG	280					
CCACCAAGG						
CTCTCTGTG						
ATTCTG						

TCGAAGTTCTGTAGGCTGAACTGATTCGCCGAAGGAAAGACGAACCATTCAGGATGCTTGATGTTATTC  
 290 300 310 320 330 340 350 360  
 300 310 320 330 340 350 360  
 TCTGAGCCGATG-CCTTGACCTTCTCTACTTTTCACTCTAGCAGTCGCAAGTCTCTGCTACTGTTTG  
 AGGACCTCAGAGAAAAGAAATGTTGAGGAAAGCATCTGTGCTTCTGAAAGAGCTGCTCTTCGAAATTA  
 370 380 390 400 410 420 430  
 TCGAAGTTCTGTAGGCTGAACTGATTCGCCGAAGGAAAGACGAACCATTCAGGATGCTTGATGTTATTC

ATGAGTCATTGGCTGATTACTTCCCTAAACATGTGAAGAGAGATGMAAAGGAATTCAACACCAAG  
440 450 460 470 480 490 500

AGAGTCACAGAAGACTTTATCAATCCACTTTTTTTTTCATTTCATATTGGCCCCCGGAGCGCATTA-----  
440 450 460 470 480 490 500

GCGAGCCTCAATTTCCTTGCCCTCACAGTGGGTGAACAATCCATTGTGGAGCTGAGGTGTGGGTGATGATGG  
510 520 530 540 550 560 570

510 520 530 540 550  
 -----GTACTTATCTGCATCTCTGGAAT-CAGGAATGCCCTGAGGTGCACAG  
 |||||  
 580 590 600 610 620 630 640  
 ACGCCTCTGAGCTGATTTGGGCTTTTCTTGATACCTCCCTAGGCGCTGGGAACCCAGCATGCAACACAC  
 560 570 580 590 600 610  
 CCCCCTTCCCCTCTTTGGGCTCTGAA-----GGGGTTTCCCTTTATGTCTTCCACCCCACTTTCCC  
 |||||  
 650 660 670 680 690 700 710 720  
 ATTCTAAGCTTTTACAGAAGACAGTAGGCTTGATGCTGCTTAAGGCTGTAACACTTACGCTTCCCTCC

620 630 640 650 660 670  
CTCCCGCCCTCTGTTTT-----GTGCCAAAAAACAAGTCTCTAAAGTTTCATGTGATTC  
|||||  
CACCCTAGAGAGAGTGGTAAACAAGCGCGTGAAGAGAAACCAATTCAGTATCACTCTGGAGAGCTTTGG  
730 740 750 760 770 780 790

[illegible]

5. US-09-477-082-2 (1-753)  
US-09-477-082-7 Sequence 7, Application US/09477082

Initial Score	=	31	Optimized Score	=	64	Significance	=	-0.07
Residue Identity	=	39%	Matches	=	69	Mismatches	=	102
Gaps	=	3	Conservative Substitutions	=			=	0

530 540 550 560 570 580 590 600  
ACGAATGCCCTGAGTGCACAGCCCTTTCCTCTTGGCGCTCAAGGGATTCTTTATGCTTCC  
CGGGTACCCCTTGGGTAAT  
X 10 20

360	370	380	390	400	410	420	430	
TACCTTTTGTCTCCCAAGCTTCCCTCGCGCTGGAAATGAGAAVACAGACCTCCCTTCTGTGACCCGTTT								
TTTAAGTTTCTTTTGCAGAGAGGAATCTTCCAAATGCAACTGATGATGACTGTGTCTGTGGAAACAGCAGG								
300	310	320	330	340	350	360		
GGAGAGTCCAGAGACTTATCATCATCCACTTTTTCCTTTTTCATTGTGGCCCTGGGGCCGACGGTTAAGT								
CCACATTTTAAGCTCTTACAGAAAGACAGTAGTGCCTTGGGTGGCTGTAAAGCTGTAAACTTAACT								
370	380	390	400	410	420	430		
ACCTTATTTCTGTCATTCTGTGTGAAATCGAATGCGAATGCGTAGGAGACAGCCCTTCCCTCTTCTGCGTCT								
440	450	460	470	480	490	500		
TTCTCCCACTTACAGAGAGTGGTTAAACAAAGGCGGTGAGAGAGAACCAATTGAGTATCACTTGGAGGC								
440	450	460	470	480	490	500		
GAAGGCGTTTCTTTTATGTGTCTTCCACCCCAACCCTTCCCTCCCTCGCTTTTGTGTGCCAAAAA								
510	520	530	540	550	560	570		
TTTGGAGAGATCTCCACCGGAGCCAGATTAAGAAATTTAGGGGCTTATTAATTAATCTATAGAAATCTTA								
510	520	530	540	550	560	570		
AGCAGCTATAAATTAATAATTT--ATTTTCAAAGTAAACATTAAGTCTAGAGGTATGCTAAATTAATAGAG								
580	590	600	610	620	630	640		
ACAGTCTCTTAACGTTTGCATGTGATGTGGGAAATTAACCTGCACCCGTTGCCAAATAAATTTT								
650	660	670	680	690	700	710		
TTTTTTGATCTGTACACTGTTTTTTAACTTT								
720	730	740	750					
TTTTTCTAAGT								

```

3. US-09-477-082-2 (1.753)
   US-09-477-082-1 Sequence 1, Application US/094770082

Initial Score = 36 Optimized score = 219 Significance = -0.03
Residue Identity = 36% Matches = 243 Mismatches = 424
Caps 5 Conservative Substitutions = 0

```

X	10	20	30	40	50	60	70
AATTGACCCGCGTATTAAAGTAAAGAACTTTCTTCGGAGCCTTTTCCACCCCTTCCCTGTCAGACA							
AAAGCGCTCCAGAACAGATTGGACGAAGGAAC-ACGGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAAGG	10	20	30	40	50	60	70
X	80	90	100	110	120	130	140
CGTGAGTTAGGACAG-GTTCAGGGGACCTCGAGACTCGATGGTCCAGGAAGGTTGGACGGGTGAATGCC							
TGGGACATCACCTCGAACACGGGGTGTCCGGACAGGGCTAAGCCAACTAAGAAATGAACACAGACCACTTCC	80	90	100	110	120	130	140
150	160	170	180	190	200	210	
TGTTGGCAGAAGTGACCTCTTTCACACGAGAAACCAATATTTTGTTCCTTGAAGCTTCTTAAGAACAGGGCT							
TCTTTTCTTTCTGACACATCTAACCCGATTTCAGCCAGGGCTGACTTTCACCAAGTCCGGCCGGAGAGGAG	150	160	170	180	190	200	210
220	230	240	250	260	270	280	
GTGGGGGTGGGGGAACAATTGATCTGCGCCCTCTGAGGACACCTGTGTGCTGCTGGCCAGGCTCTCTCTG							
GAGAGGGGTGTCTCTGTGACTTTCAGTGTCTGAGTTTATCTAAGGCAAGGAAACTCTTCTATTCCAGACCTCT	220	230	240	250	260	270	280

> O <  
O | O IntellGenetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09477082-2vs09477082-.res made by spaul on Wed 31 Mar 104 14:27:27 PST.

Query sequence being compared: US-09-477-082-2 (1-753)  
Number of sequences searched: 32  
Number of scores above cutoff: 32

Results of the initial comparison of US-09-477-082-2 (1-753) with:  
File: US09477082.seq

N	-	100-
U	-	
M	-	
U	-	
B	-	
E	-	
R	-	
O	-	
F	10-*	
S	-	
Q	-	
U	-	
E	-	
N	-	
C	-	
E	-	
S	0-*	
SCORE	0	84
STDEV	1	167
	2	251
	3	335
	4	418
	5	502
	6	586
	7	669
	8	753

PARAMETERS

Similarity matrix Unitary  
Mismatch penalty 1  
Gap penalty 5.00  
Gap size penalty 0.33  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 40 Median 13 Standard Deviation 130.74  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 6071  
Number of sequences searched: 32  
Number of scores above cutoff: 32

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Opt.	Length	Score	Sig.	Frame
---------------	-------------	------------	--------	-------	------	-------

1. US-09-477-082-2 Sequence 2, Application US 753 753 753 5.45 0  
The list of other best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
2. US-09-477-082-4 Sequence 4, Application US		659	65	216	0.19	0
3. US-09-477-082-1 Sequence 1, Application US		670	36	219	-0.03	0
4. US-09-477-082-3 Sequence 3, Application US		879	35	236	-0.04	0
5. US-09-477-082-7 Sequence 7, Application US		177	31	64	-0.07	0
6. US-09-477-082-5 Sequence 5, Application US		446	31	122	-0.07	0
7. US-09-477-082-10 Sequence 10, Application US		223	30	79	-0.08	0
8. US-09-477-082-9 Sequence 9, Application US		771	30	228	-0.08	0
9. US-09-477-082-6 Sequence 6, Application US		228	25	81	-0.11	0
10. US-09-477-082-33 Sequence 33, Application US		21	21	21	-0.15	0
11. US-09-477-082-29 Sequence 29, Application US		784	19	236	-0.16	0
12. US-09-477-082-8 Sequence 8, Application US		20	13	16	-0.21	0
13. US-09-477-082-13 Sequence 13, Application US		21	13	17	-0.21	0
14. US-09-477-082-31 Sequence 31, Application US		22	13	14	-0.21	0
15. US-09-477-082-19 Sequence 19, Application US		23	13	13	-0.21	0
16. US-09-477-082-14 Sequence 14, Application US		24	12	15	-0.21	0
17. US-09-477-082-27 Sequence 27, Application US		22	11	11	-0.22	0
18. US-09-477-082-24 Sequence 24, Application US		23	11	13	-0.22	0
19. US-09-477-082-26 Sequence 26, Application US		20	10	10	-0.23	0
20. US-09-477-082-25 Sequence 25, Application US		23	10	14	-0.23	0
21. US-09-477-082-21 Sequence 21, Application US		22	9	13	-0.24	0
22. US-09-477-082-28 Sequence 28, Application US		22	9	12	-0.24	0
23. US-09-477-082-15 Sequence 15, Application US		20	8	9	-0.24	0
24. US-09-477-082-16 Sequence 16, Application US		21	8	9	-0.24	0
25. US-09-477-082-23 Sequence 23, Application US		21	8	11	-0.24	0
26. US-09-477-082-20 Sequence 20, Application US		21	8	11	-0.24	0
27. US-09-477-082-17 Sequence 17, Application US		25	7	13	-0.25	0
28. US-09-477-082-32 Sequence 32, Application US		21	6	12	-0.26	0
29. US-09-477-082-34 Sequence 34, Application US		21	6	11	-0.26	0
30. US-09-477-082-18 Sequence 18, Application US		23	6	10	-0.26	0
31. US-09-477-082-22 Sequence 22, Application US		22	5	11	-0.27	0
32. US-09-477-082-30 Sequence 30, Application US		22	5	11	-0.27	0

1. US-09-477-082-2 (1-753)  
US-09-477-082-2 Sequence 2, Application US/09477082

Initial Score = 753 Optimized Score = 753 Significance = 5.45  
Residue Identity = 100% Matches = 753 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
AATTAGACCGGCTATTGAAAGTAAAGAAAGAAAGTCTTCTCTGAGAGCTTCCACCCCTTCCCTGCTAGCA  
AATTAGACCGGCTATTGAAAGTAAAGTAAAGTCTTCTCTGAGAGCTTCCACCCCTTCCCTGCTAGCA  
X 10 20 30 40 50 60 70  
CGTGAAGTTAGGCAAGTTAGGGAAGTCTGAGAGCTGAGAGTGGTGGAGAAAGGAGGAGGAGGAGGCT  
CGTGAAGTTAGGCAAGTTAGGGAAGTCTGAGAGCTGAGAGTGGTGGAGAAAGGAGGAGGAGGAGGCT  
X 80 90 100 110 120 130 140  
GTTGCAAGTGGGCTCTTCAACAGAAACCAATATTTTGTCTTGAAGTCTGCTAGAAACAGGGCTG  
GTTGCAAGTGGGCTCTTCAACAGAAACCAATATTTTGTCTTGAAGTCTGCTAGAAACAGGGCTG  
X 150 160 170 180 190 200 210  
GTTGCAAGTGGGCTCTTCAACAGAAACCAATATTTTGTCTTGAAGTCTGCTAGAAACAGGGCTG  
GTTGCAAGTGGGCTCTTCAACAGAAACCAATATTTTGTCTTGAAGTCTGCTAGAAACAGGGCTG  
X 220 230 240 250 260 270 280  
TGGGGGTGGGAGGAACTTGATCTGCTTGTGAGGACCTCTGAGGAGGAGGAGGAGGAGGCTGCT  
TGGGGGTGGGAGGAACTTGATCTGCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCTGCT  
X 290 300 310 320 330 340 350 360  
GTGGTTCTCTGTGAGCCGAGTCTTGTGCTTGTGCTTGTGCTGAGAGGAGTCTGAGGAGGCTGCTGCT

T  
X

30. US-09-477-082-1 (1-670)  
US-09-477-082-32 Sequence 32, Application US/09477082

Initial Score = 6 Optimized Score = 12 Significance = -0.24  
Residue Identity = 48% Matches = 12 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0

110 120 130 140 150 X 160 170  
GAGCAGGGGCTAGACCAAGTACGAATGAACCAACACACTTCCTCCTTTCTGTGACGATCTACCCGATTT  
CCATATATCTTACATTCAAAA  
X 10 20

180 190 200 210 220  
CAGCCACAGGGCTGACTTACCAGATCCGGCGGAGGAGAGAGAGGGCTGGTC  
CMA  
X

31. US-09-477-082-1 (1-670)  
US-09-477-082-13 Sequence 13, Application US/09477082

Initial Score = 5 Optimized Score = 9 Significance = -0.25  
Residue Identity = 45% Matches = 9 Mismatches = 11  
Gaps = 0 Conservative Substitutions = 0

10 20 X 30 40 X 50 60 70  
AAGCGCTCCAAGACAGATTGACAGAGACACGGGGTGGCCCACTGAATTGTGAAGAACAGGGCCAGAGAT  
GGTGGACGGGTGTGGGTG  
X 10 20

80 90  
GGGAAGTCAGCCTGAGCACGGGT

32. US-09-477-082-1 (1-670)  
US-09-477-082-31 Sequence 31, Application US/09477082

Initial Score = 5 Optimized Score = 9 Significance = -0.25  
Residue Identity = 42% Matches = 9 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

280 290 300 310 320 330 X  
CCTATTCCAGACCCCTTTGCAAGAAAGATGGCATATTACTTCCCGCCGACAGGGGTTATTATTACTAAATG  
TAGGGATTTGGAGATGTGA  
X 10 20

350 360 370 380 390  
GAGTCAGTATAATGCTTCCAAATAAAGCATGTCCAGCGCTGGGCTTT

280 290 300 310  
CTATCCGACCGCTTGCAGAGAAAGATGCATATTACTCCGCCG

22. US-09-477-082-1 (1-670)  
US-09-477-082-29 Sequence 29, Application US/09477082

Initial Score = 7 Optimized Score = 8 Significance = -0.23  
Residue Identity = 38% Matches = 8 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0

510 520 530 540 550 560 570 X  
TCCTTAGAGATTAAGTTTACCTCGAGTTCCTTGNGTGAAGTTTCTCTCTCGAGACGAGATT  
TAGGGGATTCGGAGATTGCGA X  
X 10 20

580 590 600 610 620  
CTGCCCTTAGCGTGGAGGAGGAGTTTTCACAGGTTCTCTCTTTAT

23. US-09-477-082-1 (1-670)  
US-09-477-082-17 Sequence 17, Application US/09477082

Initial Score = 7 Optimized Score = 9 Significance = -0.23  
Residue Identity = 42% Matches = 9 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 X 60 70 X  
CCGCTCCACACAGATTGACAGAGAACACAGGGGTGCACTGAATTGAGAACAGGGCCAGAGATGG  
GATGACATGTGCTTGGAAC X  
X 10 20

80 90 100 110 120  
AACTCAGCCTGAGCAGCGGTTATCCGAGCAGGGCTAAGCCAAGTACG

24. US-09-477-082-1 (1-670)  
US-09-477-082-27 Sequence 27, Application US/09477082

Initial Score = 7 Optimized Score = 12 Significance = -0.23  
Residue Identity = 50% Matches = 12 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

490 500 510 520 530 540 550  
AGTGAATCATCTCTGTTCTTAGAGATAAGTTTACCTGAGTTCTCTGAGTGAAGTTTCTCTT  
TGTCTCTCGGTAGTTTGGCTA X  
X 10 20

560 570 580 590 600 610  
TCTTCGAGAGACCAGATTCTGCCTTACGCTGAGGAGAGTGTTCACAGG

CT X

25. US-09-477-082-1 (1-670)  
US-09-477-082-25 Sequence 25, Application US/09477082

Initial Score = 6 Optimized Score = 10 Significance = -0.24  
Residue Identity = 50% Matches = 10 Mismatches = 10  
Gaps = 0 Conservative Substitutions = 0

150 160 170 180 190 X 200 210 X  
CTCTCTTTTCTGAACGATCTTACCCGCAATTCAGCAGGGGCTGACTTACCCGCGGAGGAG  
GATGACAGTGGGGGGGCTC X  
X 10 20

220 230 240 250 260

GAGAGGGCTGTCTGTACTTCAGTGTCTGAGGTTGATCAAGCCAAAG

26. US-09-477-082-1 (1-670)  
US-09-477-082-34 Sequence 34, Application US/09477082

Initial Score = 6 Optimized Score = 8 Significance = -0.24  
Residue Identity = 38% Matches = 8 Mismatches = 13  
Gaps = 0 Conservative Substitutions = 0

430 440 450 460 470 X 480 490 X  
CTCTTGAATGTTGAATTGGGCACTCTGTTCTTTAAACAGGAAATTTCTTGTTCAGATGATCAT  
CGTATCTGCATTCGAGCGG X  
X 10 20

500 510 520 530 540  
CTCTGTCTGTCTTAGAGATTAAGTTTACCTCGAGTCTCTCTGTGT

27. US-09-477-082-1 (1-670)  
US-09-477-082-30 Sequence 30, Application US/09477082

Initial Score = 6 Optimized Score = 10 Significance = -0.24  
Residue Identity = 45% Matches = 10 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

100 110 120 130 140 150 160 170  
TCCGAGAGGGCTTAAGCCAGTACGATGACACAGACACTTCTCTTTTCTGAAGATCTACCCGC  
CGTATCTCATTTGAAAGCA X  
X 10 20

180 190 200 210 220  
ATTTCAGCCACAGGGCTGACTTACCCAGTCCGCGGAGGAGAGAGAGG

28. US-09-477-082-1 (1-670)  
US-09-477-082-21 Sequence 21, Application US/09477082

Initial Score = 6 Optimized Score = 11 Significance = -0.24  
Residue Identity = 47% Matches = 11 Mismatches = 12  
Gaps = 0 Conservative Substitutions = 0

350 360 370 380 390 X 400 410  
GTGAGTAAATGCTTCCAAATAAAGATGCCGCGCTGCTTAGTTGACGTCGATGATGTCTG  
TCAATGTATTAATTACTA X  
X 10 20

420 430 440 450 460  
CCACATCCCTCTTGAATGTTGAATTGGGCATCTCTGTTCTTTAAAC

T X

29. US-09-477-082-1 (1-670)  
US-09-477-082-14 Sequence 14, Application US/09477082

Initial Score = 6 Optimized Score = 8 Significance = -0.24  
Residue Identity = 34% Matches = 8 Mismatches = 15  
Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 X 180 190  
CGAATGAACACAGACACTCTCTCTTTTCTGAACGATCTACCCGATTCAGCCAGGCTGACTTAA  
TATTTGATTAATTAATTC X  
X 10 20

X 200 210 220 230 240  
CCGAGTCCGCGGAGGAGAGAGGGGTGTTGATTCAGTGTCTGAG

TCACGAGACCAAGATTCTGCTTTAGCTGAGGAGAAAGTITTCACAGTCTCTCTCTTTATCTTTTGT  
 640 650 660 670  
 GTTTTTCAGGACCATGGGGGTTAATAAAGCGCTTT  
 X  
 TCTCTCTCTTACACCTG  
 10 20

## 14. US-09-477-082-1 (1-670)

US-09-477-082-33 Sequence 33, Application US/09477082

Initial Score = 9 Optimized Score = 10 Significance = -0.21  
 Residue Identity = 47% Matches = 10 Mismatches = 11  
 Gaps = 0 Conservative Substitutions = 0

510 520 530 540 550 560 570 X  
 TGGTTAGAGTAAGTTTACCTCGAGTCTCTGTGTGTAAGTTTCTCTTCGAGAGACAGATT  
 TAGGGGACTCGGAGACTGGCA  
 X  
 10 20

580 590 600 610 620  
 CTGCTTTACGCTGAGGAGAGTGTTCACAGGTTCTCTCTTTAT

## 15. US-09-477-082-1 (1-670)

US-09-477-082-19 Sequence 19, Application US/09477082

Initial Score = 9 Optimized Score = 13 Significance = -0.21  
 Residue Identity = 59% Matches = 13 Mismatches = 9  
 Gaps = 0 Conservative Substitutions = 0

110 120 130 140 150 160 170 X  
 AGCAGGGCTAAGGCAATGATGAACAGACCACTCTCTTTTTCAGATCTACCGCATTC  
 TTCAGCAAGTACCGCAATTC  
 X  
 10 20 X

180 190 200 210 220  
 AGCCACAGGCGCTACTTTACCCAGTCCGGGAGGAGAGAGGCGCTG

## 16. US-09-477-082-1 (1-670)

US-09-477-082-26 Sequence 26, Application US/09477082

Initial Score = 9 Optimized Score = 11 Significance = -0.21  
 Residue Identity = 47% Matches = 11 Mismatches = 12  
 Gaps = 0 Conservative Substitutions = 0

500 510 520 530 540 X 550 560  
 GTCATCTGTCTGCTTGAAGTAAGTTTACCTGCAATCTCTCTGTGAGATTCTCTCTCT  
 AGTTTCACTTTTCCAGGGCTTT  
 X  
 10 20

X 570 580 590 600 610  
 CGGAGACCAAGATTCTGCTTTACGCTGAGGAGAGTGTTCACAGGTTCT

G  
 X

## 17. US-09-477-082-1 (1-670)

US-09-477-082-23 Sequence 23, Application US/09477082

Initial Score = 8 Optimized Score = 9 Significance = -0.22  
 Residue Identity = 42% Matches = 9 Mismatches = 12  
 Gaps = 0 Conservative Substitutions = 0

560 570 580 590 600 X 610 620 X  
 CTCCTTCTCGAGACCAAGATTCTGCTTTACGCTGAGGAGAGTGTTCACAGGTTCTCTCTTTAT  
 |||||  
 |||||

TCACAGTACAGGAAAC  
 X  
 10 20

## 18. US-09-477-082-1 (1-670)

US-09-477-082-24 Sequence 24, Application US/09477082

Initial Score = 8 Optimized Score = 12 Significance = -0.22  
 Residue Identity = 54% Matches = 12 Mismatches = 10  
 Gaps = 0 Conservative Substitutions = 0

340 350 360 370 380 390 400 X  
 CTAATGAGTCAGATTAATGCTTTCCATAAAGCATGTCACGCGCTCGGCTTGTGACGTCATG  
 GGGTTGTATATCCAGACTTG  
 X  
 10 20 X

410 420 430 440 450  
 AATTGTCCACATCCCTCTTGTGAATGTTGCAATTGGGCACTCTGT

## 19. US-09-477-082-1 (1-670)

US-09-477-082-15 Sequence 15, Application US/09477082

Initial Score = 8 Optimized Score = 11 Significance = -0.22  
 Residue Identity = 50% Matches = 11 Mismatches = 11  
 Gaps = 0 Conservative Substitutions = 0

40 50 60 70 80 X 90 100 X  
 ACGGGTGCACACTGAAATTGTAAGAACAGGCGCCAGATGCGACTCAGCCTTACAGCAGGGTGTCCGG  
 GCTTACAGTGGGTAATC  
 X  
 10 20 X

110 120 130 140 150  
 AGCAGGCTAAGCAAGTACATGAACACACCACTTCTCTTTT

## 20. US-09-477-082-1 (1-670)

US-09-477-082-22 Sequence 22, Application US/09477082

Initial Score = 8 Optimized Score = 11 Significance = -0.22  
 Residue Identity = 47% Matches = 11 Mismatches = 12  
 Gaps = 0 Conservative Substitutions = 0

580 590 600 610 620 630 640 650  
 GCCTTTACGCTGAGGAGAGTGTTCACAGGTTCTCTCTTTATCTTTGTGTTTTTTCAGCCATG  
 TCCCGGTTTTCCGAGGCGGA  
 X  
 10 20

X 660 670  
 GGGGTTAATAAGCGCTTT

G  
 X

## 21. US-09-477-082-1 (1-670)

US-09-477-082-16 Sequence 16, Application US/09477082

Initial Score = 7 Optimized Score = 9 Significance = -0.23  
 Residue Identity = 45% Matches = 9 Mismatches = 11  
 Gaps = 0 Conservative Substitutions = 0

200 210 220 230 240 250 260 X  
 TCCGCGGAGGAGAGAGGCGCTGTCTGTGACTTCAGTCTGAGTTGATCAAGCAAGGAACTTC  
 CCCAACCAAGAGGTCATG  
 X  
 10 20



```
80 90 100 110 120 130 140
GGAACCTAGCCTGAGCGGCTGATCCGAGCGAGCTAGCCAGTAACTAACACGACCTTCT
GTGGGTATACATCTCGGACTCTCCAGAGAAAGATGATCCGAGCTAGCGAAGACCTCCA
60 70 80 90 100 110 120
CCTTTTTCGAGACGATCTACCCGATTTCAAGCCAGGCGTACCTTTTACCGCTCCGCGGAGGAGAA
150 160 170 180 190 200 210
AATCTTTTTCATTAATTAACAGATTCTAGTTTATTTTATTTAGTTAGT
130 140 150 160 170 180 190
GAGGCGTGTCTGTACTTCACTGCTGAGG
220 230 240
X
AAGCGCTCCAGACAGATTGC
10 20
X
```

7. US-09-477-082-1 (1-670)  
US-09-477-082-8 Sequence 8, Application US/09477082

Initial Score = 25 Optimized Score = 220 Significance = -0.08  
Residue Identity = 36% Matches = 247 Mismatches = 420  
Gaps = 13 Conservative Substitutions = 0

```
ACAAGATGGGCGAAGATCTGAGAGTCTGTGTGAAGAAATAGTAGTAATGTTCTTCGAGAAAG
60 70 80 90 100 110 120
AGAAGAAACGCGGCTGCACTGAATTTGAAGACAGGCGCAAGATGGAACAGCTGAGACGCGG
30 40 50 60 70 80 90
ACCCGATTTGGGCTGATGAGAAAGCAAGTCTTTCTAGGAGATGTTTCAATCTAGAT
130 140 150 160 170 180 190 200
TTGATC--CGAGAGCGGCTAGCCAGTACGAATGAACAGACCACTCTCTCTTTTCTGAGATCT
100 110 120 130 140 150 160
TTGACCCAGAGTACTGCTGGGTTTGTATCCAGATTTGACCAAGTTTCAAAATGAAA
210 220 230 240 250 260 270
AACCAGATTTCAAGCCAGGCTGACTTTACCCAGTCCGCGGAGGAGAGGCGTGTCTGTACTTC
170 180 190 200 210 220 230
GCAAACTCCGCGGATGACTGTGATCATCAACATTTGCAAAAGCAAGGAGAAATGCCAAA
280 290 300 310 320 330 340
AGTGTGAGTTTGAATCAAGGCAAAAGGAACTTCTATTCCTCAAGCCCTTTGCAAGAAAGATGGATAT
240 250 260 270 280 290 300
CTTCACACATTTAGGAGCAGGATGAGACACATTTGATGAGGCGGCGTCTGAGCGCTTCCA
350 360 370 380 390 400 410
ACTTGCCGCGCAGCAGGCTTATTTACTAA--ATGAGTCAATTAATGCTTCCATTAATTAACATGTC
310 320 330 340 350 360 370
AATTCCTCCCAATGAGGAAATCTCTTATGCTTATTTTAAATCAAAAGGATTTAACAATAGCTA
420 430 440 450 460 470 480
GGGCTCGGCTTATTTGACGCTCAATGATTTGCTCCACATCCCTCTCTCTGATGTTGGAAT
380 390 400 410 420 430 440
TACCAAAAGGCGCATGGTTCAGAAATGAAATTAACATATTTCCCTGAGAGTAAAGAACATTTCTA
490 500 510 520 530 540 550 560
GGGCTCTCTGTTCTTTAAACAGAACTTTCTGTCAGT--GAGTCACTCTCTTCTGCTTTAGG
450 460 470 480 490 500 510
CATTTAGTTCCTGCTTTTAAATTAATTTTAAATTAAGTATGATTAATTAATTAAT
570 580 590 600 610 620 630
520 530 540 550 560 570 580
```

```
TAAAGTTACCTGAGTTCCTCTGTGTGAATTTCTCTTCTCGGAGACAGATCTGCTTAGC
ATTAATCTTACTAAAGACATTAATAAGATTAATAGCTTTGTTGATTCATTAATCATAGCG
640 650 660 670 680 690 700
590 600 610 620 630 640 650
CTGAGGAAAGTGTTCACAGTTCCTCTTATCTTTATCTTTTGTGTTTGTGAGCCATGGGGTTAA
CTCTGTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
710 720 730 740 750 760 770
TAAAGCTTT
660 670
GGTGGGCTG
780 X
```

8. US-09-477-082-1 (1-670)  
US-09-477-082-10 Sequence 10, Application US/09477082

Initial Score = 24 Optimized Score = 80 Significance = -0.05  
Residue Identity = 37% Matches = 86 Mismatches = 137  
Gaps = 5 Conservative Substitutions = 0

```
GAACTTCCATTTCCAGACCTTTGCAAGAAAGATGCAATTAATTAATTAATTAATTAATTA
270 280 290 300 310 320 330
CTAAATGAGTATGATTAATGCTTTCGAATTAAGATGTCAGAGCGCTTATGTTGACATG
340 350 360 370 380 390 400
CGAGGCCCCCACTTCCGTCCTTCCCTCAGCCGCGCAATAGTGTGAATGTTTCAAGGCGAT
410 420 430 440 450 460 470
AATGCTGACATCCCTCTCTGATGATGTTGATGATGATGATGATGATGATGATGATGATGAT
480 490 500 510 520 530 540 550
GAAATGAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
560 570 580 590 600 610 620 630
TTCTCTTCTCTGAGACCAATCTGCTTTAGCTGG
540 550 560 570 580 590 600 610
```

9. US-09-477-082-1 (1-670)  
US-09-477-082-9 Sequence 9, Application US/09477082

Initial Score = 22 Optimized Score = 222 Significance = -0.10  
Residue Identity = 37% Matches = 255 Mismatches = 402  
Gaps = 18 Conservative Substitutions = 0

```
TGCTGCACTCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
30 40 50 60 70 80 90
AGAG---GACACGGGCTGCACTGAATTTGAAGACAGGCGCAAGATGGAATCTGAGCTGAGCA
100 110 120 130 140 150 160
AGGCGCTTTGACACGACTTTGAAGCTTCAATTTGAGATCAAGCCCGACAGTCTGACAGAGCAA
100 110 120 130 140 150 160
100 110 120 130 140 150 160
```



[illegible]

2. US-09-477-082-1 (1-670)  
US-09-477-082-3 Sequence 3, Application US/09477082

Initial Score	=	46	Optimized Score	=	222	Significance	=	0.10
Residue Identity	=	36%	Matches	=	250	Mismatches	=	418
Gaps	=	18	Conservative Substitutions	=			=	0

[illegible][illegible]

3. US-09-477-082-1 (1-670)  
US-09-477-082-2 Sequence 2, Application US/09477082

Initial Score =	36	Optimized Score =	219	Significance =	0.02
Residue Identity =	36%	Matches =	243	Mismatches =	424
Gaps =	5	Conservative Substitutions			0

X	10	20	30	40	50	60	70
AAGCGTCAAGA	CAGATTTG	AAGAGAA	-ACG	GGGTGG	CAACTG	AAATTTG	AAAGAGGCGCAAGGA
AAATTAACGCG	CGATTGAA	AGTAAAGAA	CTTTCT	CTGGAG	CCCTTCC	CCACCCCT	CTCCCTGTAGCA
X	10	20	30	40	50	60	70
80	90	100	110	120	130	140	
TGGAACTCAG	CGCTGAG	CGGGTTG	ATCCCG	AGACGGCTTA	AGCAAGAT	CAAGACAG	CACTTCC
CGTAGATTAG	GCAG-GTT	AGGAGACT	GGAGACT	GGAGCTGG	AGATGGT	CCAGAAAGG	GTGAGCGGCTGATGCC
80	90	100	110	120	130	140	
150	160	170	180	190	200	210	
TCCTTTTTC	TGAAACG	ATCTAC	CGCACTT	TCA-GCC	ACGAGGCT	CACTTAC	CCGCGCGAGAGAGAG
TGTTGCCA	AGTGGCTCT	CTTCAAC	AGAAACA	AAATTTT	GTGTTCTT	GTGACTG	CTTAACAACGGCT
150	160	170	180	190	200	210	
220	230	240	250	260	270	280	
GAGAGGCG	TGTCTG	ATTCAG	TGTGAG	GTGATG	TATCAAG	CAAGGAA	CAATCTCTATTC
GTGGGGGT	GAGAACT	TGATCT	CCCTCT	GTGAG	CACCTC	GTGGGCTG	CGTCCAGGCTCT
220	230	240	250	260	270	280	
290	300	310	320	330	340	350	
TTTCAAGAA	AGATGCA	TATTAAT	CTTGCG	CGCAGGG	GTATTTA	TCTAAAT	GTAGAGTGGTAAATAGC
TGTGTGTT	CTCTGAG	CGAGTGC	TTGATTT	GTACTTT	TCTACTG	AGACAGT	CTCCAGTTCCTCTGCG
290	300	310	320	330	340	350	
TTTCCAA	TAAAGAT	GTCCAG	CGCTCG	GGCTT	TAGTTT	GAGGTC	ATGATATTTGTGCAATCCCTCTTC

Seq id 1 vs all - to help locate primers

> O <  
O / | O  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09477082-1vs09477082-1.res made by spaul on Wed 31 Mar 104 14:25:38-EST.

Query sequence being compared: US-09-477-082-1 (1-670)  
Number of sequences searched: 32  
Number of scores above cutoff: 32

Results of the initial comparison of US-09-477-082-1 (1-670) with:  
File: US09477082.seq

N	-	100-
U	-	-
M	-	-
B	-	-
E	-	-
R	-	-
O	-	-
F	-	10-
S	-	-
E	-	5-
O	-	-
U	-	-
N	-	-
E	-	-
C	-	-
S	-	-
SCORE	0	74 149 223 298 372 447 521 596 670
STDEV	1	2

PARAMETERS

Similarity matrix Unitary 1 K-tuple 4  
Mismatch penalty 5.00 Joining penalty 30  
Gap penalty 0.33 Window size 500  
Gap size penalty 1  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 34 Median 9 Standard Deviation 116.51  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 6071  
Number of sequences searched: 32  
Number of scores above cutoff: 32

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
-----	-----	-----	-----	-----	-----	-----

1. US-09-477-082-1 Sequence 1, Application US 670 670 670 5.46 0  
The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
2. US-09-477-082-3	Sequence 3, Application US	879	46	222	0.10	0
3. US-09-477-082-2	Sequence 2, Application US	753	36	219	0.02	0
4. US-09-477-082-4	Sequence 4, Application US	659	33	210	-0.01	0
5. US-09-477-082-6	Sequence 6, Application US	228	31	80	-0.03	0
6. US-09-477-082-7	Sequence 7, Application US	177	25	62	-0.08	0
7. US-09-477-082-8	Sequence 8, Application US	784	25	220	-0.08	0
8. US-09-477-082-10	Sequence 10, Application US	223	24	222	-0.10	0
9. US-09-477-082-9	Sequence 9, Application US	771	22	220	-0.09	0
10. US-09-477-082-5	Sequence 5, Application US	448	17	130	-0.15	0
11. US-09-477-082-28	Sequence 28, Application US	22	12	12	-0.19	0
12. US-09-477-082-20	Sequence 20, Application US	21	11	14	-0.20	0
13. US-09-477-082-18	Sequence 18, Application US	21	10	15	-0.21	0
14. US-09-477-082-33	Sequence 33, Application US	21	9	10	-0.21	0
15. US-09-477-082-19	Sequence 19, Application US	22	9	11	-0.21	0
16. US-09-477-082-26	Sequence 26, Application US	23	9	13	-0.21	0
17. US-09-477-082-23	Sequence 23, Application US	21	8	9	-0.22	0
18. US-09-477-082-24	Sequence 24, Application US	22	8	12	-0.22	0
19. US-09-477-082-15	Sequence 15, Application US	22	8	11	-0.22	0
20. US-09-477-082-22	Sequence 22, Application US	23	8	11	-0.22	0
21. US-09-477-082-16	Sequence 16, Application US	20	7	9	-0.23	0
22. US-09-477-082-29	Sequence 29, Application US	21	7	8	-0.23	0
23. US-09-477-082-17	Sequence 17, Application US	21	7	9	-0.23	0
24. US-09-477-082-27	Sequence 27, Application US	24	7	12	-0.23	0
25. US-09-477-082-25	Sequence 25, Application US	20	6	10	-0.24	0
26. US-09-477-082-34	Sequence 34, Application US	21	6	8	-0.24	0
27. US-09-477-082-30	Sequence 30, Application US	22	6	10	-0.24	0
28. US-09-477-082-21	Sequence 21, Application US	23	6	11	-0.24	0
29. US-09-477-082-14	Sequence 14, Application US	23	6	8	-0.24	0
30. US-09-477-082-32	Sequence 32, Application US	25	6	12	-0.24	0
31. US-09-477-082-13	Sequence 13, Application US	20	5	9	-0.25	0
32. US-09-477-082-31	Sequence 31, Application US	21	5	9	-0.25	0

1. US-09-477-082-1 (1-670)  
US-09-477-082-1 Sequence 1, Application US/09477082

Initial Score = 670 Optimized Score = 670 Significance = 5.46  
Residue Identity = 100% Matches = 670 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X	10	20	30	40	50	60	70
AAGGCTCCAAAGACACGATTCAGAGAGAAACAGGGGTGCGCAACTGAATTGAAGAACAGGCGCAAGAT							
AAGGCTCCAAAGACACGATTCAGAGAGAAACAGGGGTGCGCAACTGAATTGAAGAACAGGCGCAAGAT							
AAGGCTCCAAAGACACGATTCAGAGAGAAACAGGGGTGCGCAACTGAATTGAAGAACAGGCGCAAGAT							
X	10	20	30	40	50	60	70
GGAGACTCAGCGCTGAGACAGCGGTTGATCCGAGCAGGCTTAAGCCAGTACGATGACAGACAGACCTTCT							
GGAGACTCAGCGCTGAGACAGCGGTTGATCCGAGCAGGCTTAAGCCAGTACGATGACAGACAGACCTTCT							
GGAGACTCAGCGCTGAGACAGCGGTTGATCCGAGCAGGCTTAAGCCAGTACGATGACAGACAGACCTTCT							
GGAGACTCAGCGCTGAGACAGCGGTTGATCCGAGCAGGCTTAAGCCAGTACGATGACAGACAGACCTTCT							
X	80	90	100	110	120	130	140
CCCTTTTTCGAAACGATCTACCCGCTTTTCAAGCCAGGCTGATCCAGAGTCCGCGGAGAGAGAGA							
CCCTTTTTCGAAACGATCTACCCGCTTTTCAAGCCAGGCTGATCCAGAGTCCGCGGAGAGAGAGA							
CCCTTTTTCGAAACGATCTACCCGCTTTTCAAGCCAGGCTGATCCAGAGTCCGCGGAGAGAGAGA							
CCCTTTTTCGAAACGATCTACCCGCTTTTCAAGCCAGGCTGATCCAGAGTCCGCGGAGAGAGAGA							
X	150	160	170	180	190	200	210
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
X	220	230	240	250	260	270	280
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
GAGGGCTGCTGTGACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT							
X	290	300	310	320	330	340	350
GCAAGAAAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT							
GCAAGAAAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT							
GCAAGAAAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT							
GCAAGAAAGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT							